

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:28 ; Search time 8184.59 Seconds

(without alignments)
819,445 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aatgcgataagtaatgta.....ggaatacccgtaacttaa 310

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Pending_Patents_NA_Main:*

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SUMMARIES				Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
Result No.	Score	Query Match	Length DB	ID	Description
1	310	100.0	310	18	US-09-423-233-7
2	302.8	97.7	534	36	US-09-961-755A-7
3	293.8	94.8	637	22	US-09-580-797-12
4	249.8	80.6	561	13	US-08-905-314-24
5	240.2	77.5	319	18	US-09-423-233-6
6	199	64.2	672	22	US-09-580-797-28
7	194.4	62.7	522	36	US-09-961-755A-8
8	194.4	62.7	522	36	US-09-961-755A-8
9	187.6	60.5	546	13	US-08-905-314-22
10	186.6	60.2	504	13	US-08-905-314-19
11	185	59.7	611	1	PCT-US98-25210-4
12	183.2	58.1	545	13	US-08-905-314-21
13	180.4	59.2	503	13	US-08-905-314-20
14	179.2	57.8	521	36	US-09-961-755A-6
15	177.8	57.4	620	22	US-09-580-797-11
16	174.2	56.2	504	18	US-09-481-293-32
17	170.8	55.1	563	22	US-09-580-797-10
18	163.8	52.8	608	1	PCT-US98-25210-3
19	161.8	45.7	392	16	US-09-241-427-3
20	140.2	45.2	599	22	US-09-580-797-37
21	139	44.8	605	1	PCT-US98-25210-1
22	138	44.5	7997	47	US-60-082-300-11599
23	136.4	44.0	597	22	US-09-580-797-35
24	136	43.9	365	18	US-09-423-233-3
25	136	43.9	617	1	PCT-US98-25210-2
26	131.4	42.4	364	18	US-09-423-233-2
27	127.2	41.0	676	22	US-09-580-797-5
28	126.6	40.8	556	1	PCT-US99-04251-7
29	126.6	40.8	556	14	US-09-037-990-7
30	125	40.3	309	18	US-09-423-233-28
31	124.4	40.1	556	13	US-08-905-314-23


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Oy 61 ttgcccgcagatattctgacgagcattcgcgttctcagcgtcatctcaaccctcaagcc 120
    |||||||
Db 401 ttgcccgcagatattctgacgagcattcgcgttctcagcgtcatctcaaccctcaagcc 460
Oy 121 cccgggttggtgttgaggatcggaagcccttgccgaagccgcccgaatctagt 180
    |||||||
Db 461 cccgggttggtgttgaggatcggaagcccttgccgaagccgcccgaatctagt 520
Oy 181 ggggttcgctgcagcttcattcgtcgtagttaaaacctgcgaactgtaagcgagcc 240
    |||||||
Db 521 ggggttcgctgcagcttcattcgtcgtagttaaaacctgcgaactgtaagcgagcc 580
Oy 241 gggcaagccgttaaaccccaactctgaatgttgacctcgagatcgatagaatc 297
    |||||||
Db 581 gggcaagccgttaaaccccaactctgaatgttgacctcgatagaatc 637

RESULT 4
US-08-905-314-24
; Sequence 24, Application US/08905314
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novartis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meligs, J. Timothy
; REGISTRATION NUMBER: 38,241
; TELECOMMUNICATION INFORMATION: CGC 1944
; TELEPHONE: (919) 541-8587
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; NAME/KEY: misc_feature
; LOCATION: 31..181
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 182..338
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: 339..504
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 505..561
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-905-314-24

Query Match      80.6%; Score 249.8; DB 13; Length 561;
Best Local Similarity 91.6%; Pred. No. 6,3e-71;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

Oy 1 aatgataaagtaatgtaattgcaaaatttaagtaatcagatcttgaagcaca 60
    |||||||
Db 232 AATGCGATGAATGAATGCAATTCGAGATTCAGTAATCATCGAATCTTGAACGCACA 291
Oy 61 ttgcccgcagatattctgacgagcattcgcgttctcagcgtcatctcaaccctcaagcc 120
    |||||||
Db 292 TTGCGCCCGCTGTATTCGGCGGCGCATGCTTTCGACGCTCATTTCAACCCCTCAAGCC 351
Oy 121 cccgggttggtgttgaggatcggaagcccttgccgaagccgcccgaatctagt 179
    |||||||
Db 352 CCCGGGTTGGTGGGATCGGCTGCTTMMGGCGGTCGCCGCCCAATATACATT 411
Oy 180 ggggttcgctgcagcttcattcgtcgtagttaaaacctgcgaactgtaagcgagcc 239
    |||||||
Db 412 GGGGTCCTGCTGCACCCCTCATTCGTAGTACCTAACCTCGCAACCTGGAACCGGCGC 471
Oy 240 gggcaagccgttaaaccccaactctgaatgttgacctcgagatcgatagaatc 299
    |||||||
Db 472 CGGCCATGCCG-TAAACCCCACTTTCATATGTTGACTTCGATCAGGTAGGAATACCC 530
Oy 300 gctgaactcaa 310
    |||||||
Db 531 GCTGAACCTAA 541

RESULT 5
US-09-423-233-6
; Sequence 6, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0-41MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6

Query Match      77.5%; Score 240.2; DB 18; Length 319;
Best Local Similarity 87.4%; Pred. No. 7,4e-68;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

Oy 1 aatgataaagtaatgtaattgcaaaatttaagtaatcagatcttgaagcaca 60
    |||||||
Db 3 aatgataaagtaatgtaattgcaaaatttaagtaatcagatcttgaagcaca 62
Oy 61 ttgcccgcagatattctgacgagcattcgcgttctcagcgtcatctcaaccctcaagcc 120
    |||||||
Db 63 ttgcccgcagatattctgacgagcattcgcgttctcagcgtcatctcaaccctcaagcc 122
Oy 121 cccgggttggtgttgaggatcggaagcccttgccgaagccgcccgaatctagt 173
    |||||||
Db 123 cccgggttggtgttgaggatcggaagcccttgccgaagccgcccgaatctagt 182

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Accession	Sequence	Position
Oy	tcgagttgcggtctcgcgcgcgcgttccttcgcgaagtaagtaaaaccccttcgaactgtac	233
Oy	174	
Db	tacagttgcggtccgcgcgcgcgttcctctgcgtaagtaagtaaaaccccttcgaactgtaga	242
Db	183	
Oy	gcgcgcgcgcgcgaagcgcgttaaaccccccaacttcgtgaatgttgacctgcgatcagttaga	293
Oy	224	
Db	gcgcgcgcgcgcgcgcgcgttaaaccccccaacttcgtgaatgttgacctgcgatcagttaga	302
Db	243	
Oy	294	
Oy	ataccgcgtgaactaa	310
Db	303	
Db	ataccgcgtgaactaa	319

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RESULT      6
US-09-580-797-28
: Sequence 28 Application US/09580797
: GENERAL INFORMATION:
: APPLICANT: Iwen, Peter C.
: APPLICANT: Hinfichs, Steven H.
: APPLICANT: Henry, Travis
: TITLE OF INVENTION: Board of Regents of the University of Nebraska
: TITLE OF INVENTION: Materials and Methods for Molecular
: FILE REFERENCE: UNNC 63149
: CURRENT APPLICATION NUMBER: US/09/580,797
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PastSeq for Windows Version 3.0
: SEQ ID NO 28
: LENGTH: 672
: TYPE: DNA
: ORGANISM: Cylindrocarpum destructans
US-09-580-797-28

```

Query Match	64.2%;	Score 199;	DB 22;	length 672;
Best Local Similarity	87.68;	Pred. No. 3.2e-54;		
Matches 241; Conservative	0;	Mismatches 30;	Indels 4;	Gaps 2

[illegible]

```

RESULT 7
US-09-961-755A-5
; Sequence 5, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
;

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```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

```

Query Match	62.7%	Score 194.4	DB 36	Length 522
Best Local Similarity	84.3%	Pred. No. 9.5e-53		
Matches 258	Conservative	0	Mismatches 36	Indels 12
				Gaps 3
QY	1	aaatcgataagtaatgtgaatttcgcaaaattcaatgaatcatcgaatctcttgaacgaca	60	
DB	229	aaatcgataagtaatgtgaatttcgcaaaattcaatgaatcatcgaatctcttgaacgaca	288	
QY	61	ttgcgcgcgcgcgaatattctgcgcgcgcgtctgttcgaagcgtcatcttcaacctcaagcc	120	
DB	289	ttgcgcgcgcgcgaatattctgcgcgcgcgtctgttcgaagcgtcatcttcaacctcaagcc	348	
QY	121	cccgagttctgtgtctgggagatcgcgaagccctctgcgcgaagccgcgcgcgaatactagt	180	
DB	349	c-----agctctgtgtctgggagatcgcgaatcaatcgcgtctcccaattgatgt	398	
QY	181	ggcgtctcgctgaagctcttcacttcgttagtagtaaaacctctgcgaactgtatgcgcgc	240	
DB	399	ggcgtctcaag-tcgagctctccataagcgtatgaataaaacctctgcgttaactgtatctgcgc	457	
QY	241	ggcgaagccggttaaacccccaactctctgaatttgcaccctgcgaatcaggtaggaaataccgc	300	
DB	458	ggcgaagccggttaaa-cccccaactctctgaatttgcaccctgcgaatcaggtaggaaataccgc	516	
QY	301	ctggaac	306	
DB	517	ctggaac	522	

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RESULT      8
US-09-961-755A-8
; Sequence 8, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ. ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ. ID NO. 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

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Query Match	62.7%	Score 194.4	DB 36	Length 522
Best Local Similarity	84.3%	Pred. No. 9,5e-53		
Matches 258	Conservative	0	Mismatches 36	Indels 12
			Gaps	3
QY	1	aatcgcgaatgaatgtgaattgcgaataatcgaatcattcgaacgaca	60	
DB	229	aaatcgcgaatgaatgtgaattgcgaattcgaatcattcgaacgaca	288	
QY	61	ttagccgccgcagatattctcggcgggcgcgcgtttcgaagcgtcatttcaacctcaagcc	120	
DB	289	ttagccgccgcagatattctcggcgggcgcgcgtttcgaagcgtcatttcaacctcaagcc	348	
QY	121	cccgagtttggtgtgttgggagatcgcgaagcccttgcgcgaagccggccgaaatctagtg	180	
DB	349	c-----agctctggtgttggtgacctcgcgaatcgaatccgcttcccccaattgattg	398	


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: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 545 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Fusarium moniliforme
: INDIVIDUAL ISOLATE: 4551
: IMMEDIATE SOURCE:
: CLONE: PCRMON1
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note="3' end of small subunit"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..178
: OTHER INFORMATION: /note="ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 179..335
: OTHER INFORMATION: /note="5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 336..488
: OTHER INFORMATION: /note="ITS 2"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 489..545
: OTHER INFORMATION: /note="5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
: US-08-905-314-21

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Query Match 59.1%; Score 183.2; DB 13; Length 545;

Best Local Similarity 83.5%; Pred. NO. 4.6e-49;

Matches 235; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

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Qy 1 aaatgcataatgaatgcaaaatcagtcgaatcatcgaatccttgaagcaca 60
Db 229 AAATGCATAATGAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 288
Qy 61 ttgcgcgcgcgaatcttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
Db 289 TTGCgcgcgcgcgaatcttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 348
Qy 121 ccggagtttggttggttggttggttggttggttggttggttggttggttggt 180
Db 349 C---AGCTTGtGTGGG-----AGCTGAGCTCCTGCTGAGTCGCCCAATTAATTG 397

```

```

Qy 181 gcggtctgcctgcagcttccattgctagtagtaaaacctgcgaactgtagcgcgcc 240
Db 398 GCGGTACG-TCGAGCTTCCATAGCGTAGTAATTTACACATCGTACGTGAATCGTGC 456
Qy 241 ggcgaagccgttaaaccccccaactctgaatgttgaccctgcgataagtaagaatccgc 300
Db 457 GGCCAGCCGCTTAA-CCCAACTTCTGAATTTGACCTCGGATGAGTAAGAAATCCGC 515
Qy 301 ctgaactaa 310
Db 516 CTGAAGTTAA 525

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RESULT 13
US-08-905-314-20
: Sequence 20, Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 503 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Fusarium graminearum
: INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546
: INDIVIDUAL ISOLATE: (consensus sequence)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..9
: OTHER INFORMATION: /note="3' end of small subunit"
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 10..155
: OTHER INFORMATION: /note="ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 156..312
: OTHER INFORMATION: /note="5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 313..466
: OTHER INFORMATION: /note="ITS 2"

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 467..503
; OTHER INFORMATION: /note="5' end of large subunit
; OTHER INFORMATION: rRNA gene"
US-08-905-314-20
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Query Match 58.2%; Score 180.4; DB 13; Length 503;
Best Local Similarity 80.0%; Pred. No. 3.7e-48;
Matches 248; Conservative 12; Mismatches 38; Indels 12; Gaps 4;

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OY 1 aatgcgataagtaagtgaattgcaaaatcagatcatcgaatcttgaagcaca 60
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DB 206 AATGCGATAAGTAAGTGAATTGCAAAATTCAGTATCAGATCAGATCTTGAAGCWSA 265
OY 61 ttgcccgcagcagatctctggcgagcagccttgctcgaagcgatcattcaaccctcaagcc 120
    |||||
DB 266 TTGCKMCKRCAGTATCTGGCGGCATCGCTGTGACGCGCATTTCAACCCCTCAAGCC 325
OY 121 cccgggttggtgtggtgggagcggaagcccttgcggaagcccgcccgaaatctagt 180
    | |||||
DB 326 C---AGVTTGGTGTGKGGAATTCAGKCC-----TTRTKACCTCCCAATAARTTG 375
OY 181 ggcgtctcgtcagccttccatctgctgaagtaaaacccctcgcaactgtagcgcgagc 240
    |||||
DB 376 GCGGTACG-TCGAACCTTCATAGCTAGTACACATCGTACTGCTATGCTGCC 434
OY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcggatcgaagtaagcaccg 300
    |||||
DB 435 GCGTACGCGGTTAA-CCCCAAGCTTGTAATGTGACCTCGGATCAGTAGAATACCCG 493
OY 301 ctgaacttaa 310
    |||||
DB 494 CTGAAGCTAA 503
```

```
RESULT 14
US-09-961-755A-6
; Sequence 6, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6
```

Query Match 57.8%; Score 179.2; DB 36; Length 521;
Best Local Similarity 83.3%; Pred. No. 9.2e-48;
Matches 255; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

```
OY 1 aatgcgataagtaagtgaattgcaaaatcagatcatcgaatcttgaagcaca 60
    |||||
DB 229 AATGCGATAAGTAAGTGAATTGCAAAATTCAGTATCAGATCAGATCTTGAAGCWSA 288
OY 61 ttgcccgcagcagatctctggcgagcagccttgctcgaagcgatcattcaaccctcaagcc 120
    |||||
DB 289 ttgcccgcagcagatctctggcgagcagccttgctcgaagcgatcattcaaccctcaagcc 348
OY 121 cccgggttggtgtggtgggagcggaagcccttgcggaagcccgcccgaaatctagt 180
    | |||||
DB 349 C---agcttggtgtggg-----agctgcagctcctgctgcactccccaataacatg 397
```

```
OY 181 ggcgtctcgtcagccttccatctgctgaagtaaaacccctcgcaactgtagcgcgagc 240
    |||||
DB 398 ggcgtctcgtcagccttccatctgctgaagtaaaacccctcgcaactgtagcgcgagc 456
OY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcggatcgaagtaagcaccg 300
    |||||
DB 457 ggcgaagccggttaaa-cccccaactctctgaatgttgactcggatcgaagtaagcaccg 515
OY 301 ctgaac 306
    |||||
DB 516 ctgaac 521
```

```
RESULT 15
US-09-580-797-11
; Sequence 11, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hintsch, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580.797
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-580-797-11
```

Query Match 57.4%; Score 177.8; DB 22; Length 620;
Best Local Similarity 84.5%; Pred. No. 2.8e-47;
Matches 251; Conservative 0; Mismatches 32; Indels 14; Gaps 4;

```
OY 1 aatgcgataagtaagtgaattgcaaaatcagatcatcgaatcttgaagcaca 60
    |||||
DB 338 AATGCGATAAGTAAGTGAATTGCAAAATTCAGTATCAGATCAGATCTTGAAGCWSA 397
OY 61 ttgcccgcagcagatctctggcgagcagccttgctcgaagcgatcattcaaccctcaagcc 120
    |||||
DB 398 ttgcccgcagcagatctctggcgagcagccttgctcgaagcgatcattcaaccctcaagcc 457
OY 121 cccgggttggtgtggtgggagcggaagcccttgcggaagcccgcccgaaatctagt 180
    | |||||
DB 458 C---agcttggtgtggg-----cgtaactgcgtccccaatctagt 505
OY 181 ggcgtctcgtcagccttccatctgctgaagtaaaacccctcgcaactgtagcgcgagc 240
    |||||
DB 506 ggcgtcagc-tcgaactcctcagtagcgtgaagtaaaacccctcgtactgtagcgtcgc 564
OY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcggatcgaagtaagcaccg 297
    |||||
DB 565 ggcgaagccggttaa-cccccaactctctgaatgttgactcggatcgaagtaagcaccg 620
```

Search completed: August 22, 2002, 00:39:29
Job time: 13054 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:49 ; Search time 663.62 Seconds

(Without alignments)
1256.889 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aatgcgataagtaagtga.....ggataccgcgtgaacttaa 310

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1721111 seqs, 1345317543 residues

Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending-Patents-NA-New:*
1: /cgn2_6/ptodata/2/pna/PCr_NEM_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEM_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEM_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEM_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEM_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEM_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEM_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEM_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	310	100.0	310	7	US-10-046-955-7
2	240.2	77.5	319	7	US-10-046-955-6
3	136.2	43.9	652	1	PCT-US02-11769-2
4	136	43.9	365	7	US-10-046-955-3
5	131.4	42.4	364	7	US-10-046-955-2
6	125	40.3	309	7	US-10-046-955-28
7	124.6	40.2	641	5	US-09-766-173C-4
8	124.4	40.1	536	5	US-09-517-790-5
9	124.2	40.1	650	1	PCT-US02-11769-4
10	123.2	39.7	365	7	US-10-046-955-5
11	120.2	38.8	618	5	US-09-766-173C-5
12	111.6	36.0	343	7	US-10-046-955-27
13	111.6	36.0	344	7	US-10-046-955-26
14	108.8	35.1	336	7	US-10-046-955-29
15	107.8	34.8	346	7	US-10-046-955-25
16	107.4	34.6	515	5	US-09-517-790-1
17	107.4	34.6	523	5	US-09-517-790-4
18	107.2	34.6	346	7	US-10-046-955-24
19	100.2	32.3	355	7	US-10-046-955-4
20	92.8	29.9	516	5	US-09-517-790-2
21	91.2	29.4	570	5	US-09-517-790-3
22	60.8	19.6	330	7	US-10-046-955-8
23	59.4	19.2	327	7	US-10-046-955-10
24	59.4	19.2	328	7	US-10-046-955-9
25	59.4	19.2	330	7	US-10-046-955-12

26	53.6	17.3	322	7	US-10-046-955-11	Sequence 11, Appl
27	53	17.1	131	5	US-09-975-254-5041	Sequence 5041, Ap
28	53	17.1	250	5	US-09-975-254-4556	Sequence 4556, Ap
29	53	17.1	3927	7	US-10-155-881-16180	Sequence 16180, A
30	52	16.8	1180	7	US-10-155-881-2120	Sequence 2120, Ap
31	52	16.8	1414	7	US-10-155-881-6537	Sequence 6537, Ap
32	51.4	16.6	486	7	US-10-046-955-19	Sequence 19, Appl
33	50.4	16.3	2091	5	US-09-935-625-5545	Sequence 5545, Ap
34	50.4	16.3	2091	5	US-09-935-625-17457	Sequence 17457, A
35	50.4	16.3	2091	5	US-09-935-625-25792	Sequence 25792, A
36	50.4	16.3	2097	5	US-09-935-625-5599	Sequence 5599, Ap
37	50.4	16.3	2097	5	US-09-935-625-6116	Sequence 6116, Ap
38	50.4	16.3	2097	5	US-09-935-625-17511	Sequence 17511, A
39	50.4	16.3	2097	5	US-09-935-625-18547	Sequence 18547, A
40	50.4	16.3	2097	5	US-09-935-625-25913	Sequence 25913, A
41	50.4	16.3	2097	5	US-09-935-625-26950	Sequence 26950, A
42	50.4	16.3	4310	7	US-10-177-253-71	Sequence 71, Appl
43	50	16.1	1037	7	US-10-155-881-2313	Sequence 2313, Ap
44	50	16.1	3480	8	US-60-391-781-202	Sequence 202, App
45	49.8	16.1	1351	7	US-10-155-881-6113	Sequence 6113, Ap

ALIGNMENTS

RESULT 1
US-10-046-955-7
Sequence 7, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilianna
APPLICANT: Choi, Jong Soo
TITLE OR INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-7
Query Match 100.0%; Score 310; DB 7; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.4e-93;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 aatgcgataagtaagtgaatgcgaatgcgtgaatcatcatgaatctttgaagcaca 60
Db 1 aatgcgataagtaagtgaatgcgaatgcgtgaatcatcatgaatctttgaagcaca 60
QY 61 ttgcgcgcgcgaatctctgtgcgcgcgcgtcttgagcgtcatcttcaaccctcaagcc 120
Db 61 ttgcgcgcgcgaatctctgtgcgcgcgcgtcttgagcgtcatcttcaaccctcaagcc 120
QY 121 ccgcggttggttggttggttggttggttggttggttggttggttggttggttggttggt 180
Db 121 ccgcggttggttggttggttggttggttggttggttggttggttggttggttggttggt 180
QY 181 gcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgc 240


```

: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus niger
US-10-046-955-3

```

Query Match	43.98;	Score 136;	DB 7;	Length 365;
Best Local Similarity	69.08;	Pred. No. 3.7e-35;		
Matches 218; Conservative	0;	Mismatches 90;	Indels 8;	Gaps 2

OY	1	aaatcgcgaatgaatgaaatttgcgaataatcgaatgaaatttgcgaagcga	60
Db	52	aaatgcgaataactaatcgtgaattcgaataatcgaatgcgaattcgcgaacgca	111
OY	61	ctgcgcgccgcgaattctctgcgcggcaltgcctgtctcgaacgalttcaacctcaagcc	120
Db	112	ctgcgcgccgcggaattctcgcggcgctgcctgtctcgaacgaltcgtctgcctcgaag--	169
OY	121	cccggaattctgtatctgcggatcgcgaagccctctgcgcgaacgcggcccggaattagt	180
Db	170	cacgcgctctgtctgtctgcgcgtcccccctctccgcggggagcgggcccgaagcagcg	229
OY	181	gcgcgtctgcgcagcttccattgcgta-----gtatgaaaaccttcgcgaactgtatcg	234
Db	230	gcgcgaacgcgcgtccgatcctctcgaagcgtatgcggcttcttcacccctgtctgtcgaagccgcgc	289
OY	235	cgcggcgcgcgaacgcgtaataaaccccccaactctgtaatttaccctcggaatacgaatgaata	294
Db	290	cggcgccctgcgcgaagctatcccaaccattttctccaggtcgaactcgcgaatcagaatgaagga	349
OY	295	taaccgcgtgaacttaa	310
Db	350	taaccgcgtgaacttaa	365

```

RESULT 5
US-10-046-955-2
: Sequence 2, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT:
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aidorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 364
: TYPE: DNA
: ORGANISM: Aspergillus fumigatus
US-10-046-955-2

```

Query Match	42.48;	Score 131.4;	DB 7;	Length 364;
Best Local Similarity	68.18;	Pred. No. 1.3e-33;		
Matches 213; Conservative	0;	Mismatches 96;	Indels 4;	Gaps 2

OY	1	aaagcgatgaagaagtgaattgcgcaaatcctgcgtgaatcatctgaattcttgaagccaca	60
Dd	52	aactcgataaacctaactgatgtgaattgcgagaatttcggtgaatatcatgaaattctttgaacgaca	111
OY	61	tctgcgccgcaccagtattctctgcgcggcatgctctgtcttgagcgtcatcttcaaccctcaagcc	120
Dd	112	tctgcgcacctgttatctccggcggggcatgctctgtctcgaggcgtcatgtgtctgcacatca -ag	170
OY	121	cctcgagtttgtggtgttgaggatcgcgcaagccctctgcgcgcaagccgcgcccgaaatctcagt	180
Dd	171	caecgagctctgtgtcttgaggcccccccctccctcccccggggagcgagcccgaaaagcgagcg	230
OY	181	gcgcgtctgcctgcagctcttcattgcgtla--gtfagihaaacccctgcgaactgttacgcgg	237
Dd	231	gcgcgcacccgcgtctcctcctcgagcgtatcgggcctgtccctgcctctgtaggccccgcgc	290
OY	238	cgcgcgccaagccgcttcaaaccccccaactcttgaaftgttgcacctctggtcttcaggatgaatc	297
Dd	291	ggcgcgcagcgcgacaccaacttatcttcttaaggtctgaacctcgcgtlccaggtlagggatcac	350
OY	298	ccgctggaacttaa	310
Dd	351	ccgctggaacttaa	363

```

RESULT 6
US-10-046-955-28
: Sequence 28, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Etrol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 28
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Penicillium notatum
US-10-046-955-28

```

	Query Match	40.3%	Score 125;	DB 7;	Length 309;
	Best Local Similarity	69.0%	Pred. No. 1,6e-31;		
	Matches 216;	Conservative	0;	Mismatches 90;	Indels 7; Gaps 3;
QY	1 aaatgcacataagaaatgaattcagaataaacatcgagaaatcatgcaatcttgaaacaca				
Db	1 aaatgcacatacgaaaagtcgaatttc-aaattccaagtaactcgaagtctttgaaccaca				
QY	61 ttgcgccgcgcgaattatctcgcgggcacagctgttctgcagcattcataaccacgaacc				
Db	60 ttgcgcccccttgttatctccgcgggggcacgcctgcgttcgcagcgctatctgtcctctaagca				
QY	121 ccgcggattgtgtgtgtgggaaatcgagcaagcccttgcgcgaacgcgcgcgcgaatatctagt				
Db	120 c---ggctctgtgtgtgtgtggccccgcctccatcccgcggqaaacagccccaataatgcacac				

[illegible]

```

RESULT 7
US-09-766-173C-4
: Sequence 4: Application US/09766173C
: GENERAL INFORMATION:
: APPLICANT: Carroll, George C.
: TITLE OF INVENTION: Materials and Methods For detection of
: TITLE OF INVENTION: Pathogenic Gulgnardia Citricarpa
: FILE REFERENCE: Oregon 99-09
: CURRENT APPLICATION NUMBER: US/09/766,173C
: CURRENT FILING DATE: 2001-01-22
: PRIOR APPLICATION NUMBER: PCT/US01/01735
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/177,013
: PRIOR FILING DATE: 2000-01-19
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 641
: TYPE: DNA
: ORGANISM: Gulgnardia Citricarpa
US-09-766-173C-4

```

Query Match	40.28;	Score 124.6;	DB 5;	Length 641;
Best Local Similarity	64.68;	Pred. No. 2.8e-31;		
Matches 201; Conservative	0;	Mismatches 109;	Indels 1;	Gaps 1;

```

OY      1  aatgcgtaagtaatgtaattgcgaattcgaataatcaatgaatcaatcgaattcttgaagcaca 60
          |||||
Db      318  aatgcgtaagtaatgtaattgcgaattcgaataatcaatgaatcaatcgaattcttgaagcaca 377
OY      61  ttgcgcgccgcagatattctgcggtgcggtcctgtctgcagcgltcaattcaacccttaagcc 120
          |||||
Db      378  ttgcgcgccgcagatattctgcggtgcggtcctgtctgcagcgltcaattcaacccttaagcc 437
OY      121  ccgcggttgcgtgttcggtgatcgcgcgaagcccttcgtgcgcgaagccgcgc-ccgaatctagt 179
          |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      438  ctgccttcgltatgcgcgcgtccgcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 497
OY      180  ggcggtcctgcgtcagctctccattgcgtagtagtaaaacccctgcgaactcgtgcgcgcgc 239
          |  ||||
Db      498  ctgcgcctcgcgcgtagtagtaaaatatactcgccttcgtagagagaggggcgcgtgcgcgcgc 557
OY      240  cgcgcgaagcgcgttaaaccccccaacttcgaaatglttgacctcgcgatcagtaggaataccc 299
          |||||
Db      558  gacacatgcgaccttcgtcactattttcccaaggtgcacctcgcgatcagtagggatataccc 617
OY      300  gctgaacttaa 310
          |||||
Db      618  gctgaacttaa 628

RESULT      8
US-09-517-790-5
; Sequence 5, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of F
; FILE REFERENCE: RU-0093

```

```

? CURRENT APPLICATION NUMBER: US-09/517,790
?
? CURRENT FILING DATE: 2000-03-02
? PRIOR APPLICATION NUMBER: US 60/123,099
? PRIOR FILING DATE: 1999-03-05
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: PatentIn version 3.1
?
? SEQ ID NO 5
?
? LENGTH: 536
? TYPE: DNA
? ORGANISM: Amapelomyces humuli
US-09-517-790-5
```

Query Match	40.1%;	Score 124.4;	DB 5;	Length 536;
Best Local Similarity	69.4%;	Pred. No. 3e-31;		
Matches 215; Conservative	0;	Mismatches 86;	Indels 9;	Gaps 3;

QY	1	aagcgcaatgaatctgaaattgcgaatctgaatcatcgaatcctttgaagcaca	60
Db	220	aaatgcgataaagctgctgtgtaattgcgaatctcaatctgaatacctcttgaacgcaca <td>2179</td>	2179
QY	61	ttgcgcgccgcagatctctcgcgcgacatgcctgtctcgagctcatcttcaaccctcaagcc <td>120</td>	120
Db	280	ttgcgcacctctgtaattcgaaggcgatgcctgtctcgagctcatcttgccttcaag-- <td>3377</td>	3377
QY	121	cccgagtttggttgtctggagatcgcaagcccttcggcgaagccgcccgcgaatactagtg <td>180</td>	180
Db	338	ctctgccttggtggtgtgttcttcgctctcgcgcgtgtgatacctgcgctccaataacatg <td>357</td>	357
QY	181	ggcgtctcgcctgcagcttccatctgctgtagtaagtaaaacctcgcaactggtlaacgcgcg <td>240</td>	240
Db	398	gcaacgcgcgcgattgaaattcgcgaagcgcaagt----acatctcgcgccttgcacatcaaac <td>452</td>	452
QY	241	ggccaaagccgttaaaccccccaactctggaatgtgtgacctctggaatcgaatgagataaccg <td>300</td>	300
Db	453	gacgacgtc--caaaagtacatcttttaccactcttgacctcgtgatcgcgtgtgggataaccg <td>510</td>	510
QY	301	ctgaacttaa 310 <td></td>	
Db	511	ctgaacttaa 520 <td></td>	

```

RESULT      9
PCT-US02-11769-4
; Sequence 4, Application PC/TUS0211769
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manke, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: PCT/US02/11769
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Muscodor roseus
; PCT-US02-11769-4

```

Query Match	40.1%	Score 124.2	DB 1	Length 650
Best Local Similarity	71.4%	Pred No. 3	Ge-31	
Matches 222	Conservative	0	Mismatches 78	Indels 11
			Gaps 4	

OY	1	aatgcgataagtaatgtaattgcgaataatcagtcgatcatcgaaatccttgaacgcaca	60
Db	329	aaatgcgataaagtaatgtaattgcgaataatcagtcgatcatcgaaatccttgaacgcaca	388

[illegible]

```

: RESULT 10
: US-10-046-955-5
: Sequence 5, Application US/10046595
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Etrol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Chol, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423, 233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
: US-10-046-955-5

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Query Match	39.78;	Score 123.2;	DB 7;	Length 365;
Best Local Similarity	66.58;	Pred. NO. 6.8e-31;		
Matches 210; Conservative	0;	Mismatches 98;	Indels 8;	Gaps 2

Oy	1	aatgacgataaagtaatgaaattgcaaatcaatgataatcgaatcttgaagaca	60
Db	52	aactgcgataaagataatgaaatgcagaataatcagatgataatcgaatcttgaagaca	111
Oy	61	ttagcgcgcgcgcgaattctctgcgagacatgcctgtctcagacgtcatttcaacccctcaagcc	120
Db	112	ttagcgcgcgcgcgcgaattctctgcgagacatgcctgtctcagacgtcatttctgctcctaag--	169
Oy	121	cccgagcttgcgtctgcgagatcgcgaacgccctctgcgacgaacccgcgcgaatactaatg	180
Db	170	cccgagcttgcgtctgcgagatcgcgaacgccctctgcgacgaacccgcgcgaatactaatg	229
Oy	181	gagcgtctgcgtctgcgaatctccatctgcgtatgataaaccctctgcg-----aactgtaacg	234
Db	230	cgcgaacccgcgtctccctctgcgacgataagggctctgtgcacacccctcgaattagagccgcgc	289

OY 235 cggcgccgacgaagcgcgttaaaccccccaactcttgaagtgtgactcgtgatcagtagtaa 294
 ||||| | | | | | | |
db 290 gggcgccacgacggcgcttcaccacaactatcttcacagttcgacctcgatccaagttagga 349
 ||||| | | | | | | |
OY 295 taaccgctgaacttaa 310
 ||||| | | | | | | |
db 350 taaccgctgaacttaa 365

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RESULT 11
US-09-766-173C-5
; Sequence 5, Application US/09766173C
; GENERAL INFORMATION:
; APPLICANT: Carroll, George C.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Pathogenic Guignardia Citricarpa
; FILE REFERENCE: Oregon 99-09
; CURRENT APPLICATION NUMBER: US/09/766,173C
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/177,013
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Guignardia Citricarpa
US-09-766-173C-5

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Query Match	38.8%	Score 120.2	DB 5	Length 618
Best Local Similarity	66.5%	Pred. No. 7.9e-30		
Matches 208	Conservative	0	Mismatches 93	Indels 12
				Gaps 2

[illegible]

RESULT 12
US-10-046-955-27
; Sequence 27, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Etrol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:49 : Search time 2238.68 Seconds
(without alignments)
168.259 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18
Sequence: 1 tctatgacgctcgcct 18

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: GenEmbl:*
2: gb_da:*
3: gb_htg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	16.4	91.1	310	8	AF117922	AF117922 Gibberella
2	16.4	91.1	351	8	AF162903	AF162903 Fusarium
3	16.4	91.1	419	8	AF11060	AF11060 Fusarium
4	16.4	91.1	457	8	AF261745	AF261745 Cylindroc
5	16.4	91.1	458	8	AF008562	AF008562 Fusarium
6	16.4	91.1	464	8	AF261740	AF261740 Calonectr
7	16.4	91.1	466	8	AF261740	AF261740 Calonectr
8	16.4	91.1	466	8	NGA228662	AJ228662 Nectria g
9	16.4	91.1	466	8	NGA228663	AJ228663 Nectria g
10	16.4	91.1	466	8	NGA228664	AJ228664 Nectria g
11	16.4	91.1	466	8	NGA228665	AJ228665 Nectria g
12	16.4	91.1	466	8	NGA228666	AJ228666 Nectria g
13	16.4	91.1	466	8	NGA228667	AJ228667 Nectria g
14	16.4	91.1	466	8	NGA228668	AJ228668 Nectria g
15	16.4	91.1	466	8	NGA228669	AJ228669 Nectria g
16	16.4	91.1	466	8	NGA228670	AJ228670 Nectria g
17	16.4	91.1	466	8	NGA228671	AJ228671 Nectria g
18	16.4	91.1	466	8	NGA228672	AJ228672 Nectria g
19	16.4	91.1	466	8	NGA228673	AJ228673 Nectria g
20	16.4	91.1	466	8	NGA228674	AJ228674 Nectria g
21	16.4	91.1	466	8	NGA228675	AJ228675 Nectria g
22	16.4	91.1	466	8	NGA228676	AJ228676 Nectria g
23	16.4	91.1	466	8	NGA228677	AJ228677 Nectria g
24	16.4	91.1	466	8	NGA228678	AJ228678 Nectria g
25	16.4	91.1	466	8	NGA228679	AJ228679 Nectria g
26	16.4	91.1	466	8	NGA228680	AJ228680 Nectria g
27	16.4	91.1	466	8	NGA228681	AJ228681 Nectria g
28	16.4	91.1	466	8	NGA228682	AJ228682 Nectria g
29	16.4	91.1	466	8	NGA228683	AJ228683 Nectria g
30	16.4	91.1	466	8	NGA228684	AJ228684 Nectria g
31	16.4	91.1	466	8	NGA228685	AJ228685 Nectria g
32	16.4	91.1	466	8	NGA228686	AJ228686 Nectria g
33	16.4	91.1	466	8	NGA228687	AJ228687 Nectria g
34	16.4	91.1	466	8	NGA228688	AJ228688 Nectria g
35	16.4	91.1	466	8	NGA228689	AJ228689 Nectria g
36	16.4	91.1	466	8	NGA228690	AJ228690 Nectria g
37	16.4	91.1	466	8	NGA228691	AJ228691 Nectria g
38	16.4	91.1	466	8	NGA228692	AJ228692 Nectria g
39	16.4	91.1	469	8	NRA7353	AJ007353 Nectria r
40	16.4	91.1	470	8	AF132800	AF132800 Fusarium
41	16.4	91.1	470	8	AF440528	AF440528 Fusarium
42	16.4	91.1	470	8	AF440530	AF440530 Fusarium
43	16.4	91.1	470	8	AF440543	AF440543 Fusarium
44	16.4	91.1	470	8	AF440551	AF440551 Fusarium
45	16.4	91.1	471	8	AF150468	AF150468 Nectria h

ALIGNMENTS

RESULT 1
AF117922 310 bp DNA linear PLN 17-JUN-2000
LOCUS Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial
DEFINITION sequence: Internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.

ACCESSION AF117922
VERSION AF117922
KEYWORDS AF117922.1 GI:8570108
SOURCE Gibberella fujikuroi.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE 1 (bases 1 to 310)
AUTHORS Choi,J.S., Westernman,J.M. and Morrison,C.J.
TITLE Rapid differentiation of filamentous fungi using species-specific
DNA probes
JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE 2 (bases 1 to 310)
AUTHORS Choi,J.S., Westernman,J.M. and Morrison,C.J.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

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FEATURES
  source
    1..310
      /organism="Gibberella fujikuroi"
      /strain="ATCC 38519"
      /db_xref="ATCC:38519"
      /db_xref="taxon:5127"
      <1..159
      /product="5.8S ribosomal RNA"
      159..272
      /note="ITS2"
      /product="internal transcribed spacer 2"
      273..>310
      /product="28S ribosomal RNA"
      73 a      86 c      80 g      71 t
BASE COUNT
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Query Match
Best Local Similarity 94.4% Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctatgacggtctcgct 18
    ||||| |||||
Db 174 TCTAGTGGCGCTCTCGCT 191

RESULT 2
AF162903 351 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence;
            internal transcribed spacer 2, complete sequence; and 28S ribosomal
            RNA gene, partial sequence.
ACCESSION AF162903
VERSION AF162903.1 GI:5690392
KEYWORDS
SOURCE
ORGANISM
Fusarium proliferatum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE
  1 (bases 1 to 351)
AUTHORS
  Min,B.R.
TITLE
  Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
JOURNAL
  Dong, Chong No-cu, Seoul 110-743, Korea
FEATURES
  source
    1..351
      /organism="Fusarium proliferatum"
      /strain="6787"
      /db_xref="taxon:42674"
      <1..128
      /product="5.8S ribosomal RNA"
      129..293
      /product="internal transcribed spacer 2"
      294..>351
      /product="28S ribosomal RNA"
      87 a      94 c      94 g      76 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 94.4% Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctatgacggtctcgct 18
    ||||| |||||
Db 195 TCTACTGGCGCTCTCGCT 212

RESULT 3
AF111060 419 bp DNA linear PLN 20-JAN-1999
LOCUS
DEFINITION Fusarium subglutunum var. subglutunum strain BBA62431 internal
            transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,

```

```

complete sequence; and internal transcribed spacer 2, partial
sequence.
AF111060
AF111060.1 GI:4160484
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium subglutunum var. subglutunum.
Fusarium subglutunum var. subglutunum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
  1 (bases 1 to 419)
AUTHORS
  Bulat,S.A., Yli-Mattila,T. and Alekhina,I.A.
TITLE
  Molecular taxonomy of Fusarium strains by means of ribotyping, rDNA
  sequencing and up-PCR analysis. A case study of Sporotrichiella
  section
JOURNAL
  Unpublished
  2 (bases 1 to 419)
REFERENCE
  Bulat,S.A. and Alekhina,I.A.
AUTHORS
  Direct Submission
  Submitted (03-DEC-1998) Department of Molecular and Radiation
  Biophysics, Petersburg Nuclear Physics Institute RAS, Gatchina,
  Leningrad Region 188350, Russia
FEATURES
  source
    1..419
      /organism="Fusarium subglutunum var. subglutunum"
      /strain="BBA62431"
      /variety="subglutunum"
      /db_xref="taxon:86548"
      <1..136
      /note="ITS1"
      /product="internal transcribed spacer 1"
      137..294
      /product="5.8S ribosomal RNA"
      295..>419
      /note="ITS2"
      /product="internal transcribed spacer 2"
BASE COUNT 105 a 118 c 98 g 98 t
ORIGIN

Query Match
Best Local Similarity 94.4% Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctatgacggtctcgct 18
    ||||| |||||
Db 365 TCTAGTGGCGCTCTCGCT 382

RESULT 4
AF261745 457 bp DNA linear PLN 26-SEP-2000
LOCUS
DEFINITION Cyllindrocladiella parva internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence.
ACCESSION AF261745
VERSION AF261745.1 GI:10304122
KEYWORDS
SOURCE
ORGANISM
Cyllindrocladiella parva.
Cyllindrocladiella parva
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Cyllindrocladiella.
REFERENCE
  1 (bases 1 to 457)
AUTHORS
  Risede,J.-M. and Simoneau,P.
TITLE
  Typing Cyllindrocladium species by analysis of ribosomal DNA spacers
  polymorphism: application to field isolates issued from banana
  rhizosphere
JOURNAL
  Unpublished
  2 (bases 1 to 457)
REFERENCE
  Risede,J.-M. and Simoneau,P.
AUTHORS
  Direct Submission
  Submitted (28-APR-2000) Plant Pathology, Universite d'Angers, 2 Bd
  Lavoisier, Angers 49045, France
FEATURES
  Location/Qualifiers

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source      1. .457
            /organism="Cylindrocloadiella parva"
            /strain="MUC1 636"
            /db_xref="taxon:137496"
misc_RNA    1. .128
            /product="Internal transcribed spacer 1"
            129. .296
            /product="5.8S ribosomal RNA"
misc_RNA    297. .457
            /product="Internal transcribed spacer 2"
BASE COUNT 101 a 133 c 109 g 114 t
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Query Match 91.1%; Score 16.4; DB 8; Length 457;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgt 18
    ||||| ||||| |||||
Db 366 TCTAGTGGCGCTCTCGCT 383

RESULT 5
AF008562 458 bp DNA linear PLN 07-JUN-1999
LOCUS Fusarium redolens internal transcribed spacer 1, partial sequence,
DEFINITION 5.8S ribosomal RNA gene, complete sequence, and internal
transcribed spacer 2, partial sequence.
ACCESSION AF008562
VERSION AF008562.1 GI:4102047
KEYWORDS
SOURCE
ORGANISM Fusarium redolens.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; Mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 458)
AUTHORS Paavanan-Huhtala,S., Hyvonen,J., Bula,S.A. and Yli-Mattila,T.
TITLE RAPD-PCR, isozyme, rDNA RFLP and rDNA sequence analyses in
identification of Finnish Fusarium oxysporum isolates
JOURNAL Mycol. Res. 103 (5), 625-634 (1999)
REFERENCE 2 (bases 1 to 458)
AUTHORS Yli-Mattila,T., Paavanan-Huhtala,S. and Hyvonen,J.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1997) Lab. of Plant Physiology and Molecular
Biology, Dept. of Biology, Univ. of Turku, Turku 20014, Finland
FEATURES
source      1. .458
            /organism="Fusarium redolens"
            /strain="93139"
            /db_xref="taxon:48865"
            /note="isolated from barley root in Siuntio in Finland in
            1985"
misc_RNA    <1. .134
            /product="Internal transcribed spacer 1"
            135. .293
            /product="5.8S ribosomal RNA"
misc_RNA    294. .>458
            /product="Internal transcribed spacer 2"
BASE COUNT 115 a 130 c 106 g 104 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 458;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgt 18
    ||||| ||||| |||||
Db 360 TCTAGTGGCGCTCTCGCT 377

RESULT 6

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```

AF261740
LOCUS AF261740 464 bp DNA linear PLN 26-SEP-2000
DEFINITION Calonectria kytensis strain ATCC22677 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF261740
VERSION AF261740
KEYWORDS AF261740.1 GI:10304117
SOURCE
ORGANISM Calonectria kytensis.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; Nectriaceae; Calonectria.
REFERENCE 1 (bases 1 to 464)
AUTHORS Risede,J.-M. and Simoneau,P.
TITLE Typing Cylindrocloadium species by analysis of ribosomal DNA spacers
polymorphism: application to field isolates issued from banana
rhizosphere
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Risede,J.-M. and Simoneau,P.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2000) Plant Pathology, Universite d'Angers, 2 Bd
Lavoisier, Angers 49045, France
FEATURES
source      1. .464
            /organism="Calonectria kytensis"
            /strain="ATCC22677"
            /db_xref="ATCC:22677"
            /db_xref="taxon:40623"
            1. .128
            /product="Internal transcribed spacer 1"
            129. .297
            /product="5.8S ribosomal RNA"
misc_RNA    298. .464
            /product="Internal transcribed spacer 2"
BASE COUNT 110 a 132 c 107 g 115 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 464;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgt 18
    ||||| ||||| |||||
Db 371 TCTAGTGGCGCTCTCGCT 388

RESULT 7
NGA228662 466 bp RNA linear PLN 01-FEB-1999
LOCUS Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
DEFINITION gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS
100318).
ACCESSION AJ228662
VERSION AJ228662.1 GI:4210757
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE
ORGANISM Neonectria galligena.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; Nectriaceae; Neonectria.
REFERENCE 1 (bases 1 to 466)
AUTHORS Langreil,S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langreil, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5NH, UNITED KINGDOM
REFERENCE 2 (bases 1 to 466)
AUTHORS Langreil,S.R.H.
JOURNAL Unpublished
FEATURES
Location/Qualifiers

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/isolate="CBS 100318"
/db_xref="taxon:56674"
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5..139
/note="Internal transcribed spacer 1 (ITS 1)"
140..297
/gene="5.8S rRNA gene"
140..297
/gene="5.8S rRNA gene"
298..462
/note="Internal transcribed spacer 2 (ITS 2)"
463..>466
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BASE COUNT 107 a 142 c 111 g 106 t
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Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tctagtacggtctgcgt 18
||||| |||||||
Db 365 TCTAGTGGCGGTCTGCCT 382

RESULT 8
NGA228663 466 bp rRNA linear PLN 01-FEB-1999
LOCUS
DEFINITION Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS
100317).
ACCESSION AJ228663
VERSION AJ228663.1 GI:4210758
KEYWORDS 18S ribosomal RNA; 5.8S rRNA gene; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE Neonectria galligena.
ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE 1 (bases 1 to 466)
Langrell,S.R.H.
AUTHORS Direct Submission
TITLE Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
JOURNAL 2 (bases 1 to 466)
Langrell,S.R.H.
FEATURES
location/Qualifiers
source 1..466
/organism="Neonectria galligena"
/isolate="CBS 100317"
/db_xref="taxon:56674"
<1..4
/gene="18S rRNA gene"
1..4
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5..139
/gene="18S rRNA gene"
misc_RNA 5..139
/note="Internal transcribed spacer 1 (ITS 1)"
140..297
/gene="5.8S rRNA gene"
140..297
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298..462
/gene="5.8S rRNA gene"
misc_RNA 298..462

RNA /note="Internal transcribed spacer 2 (ITS 2)"
463..>466
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463..466
/gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tctagtacggtctgcgt 18
||||| |||||||
Db 365 TCTAGTGGCGGTCTGCCT 382

RESULT 9
NGA228664 466 bp rRNA linear PLN 01-FEB-1999
LOCUS
DEFINITION Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL
40716).
ACCESSION AJ228664
VERSION AJ228664.1 GI:4210759
KEYWORDS 18S ribosomal RNA; 5.8S rRNA gene; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE Neonectria galligena.
ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE 1 (bases 1 to 466)
Langrell,S.R.H.
AUTHORS Direct Submission
TITLE Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
JOURNAL 2 (bases 1 to 466)
Langrell,S.R.H.
FEATURES
location/Qualifiers
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/db_xref="taxon:56674"
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5..139
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/note="Internal transcribed spacer 1 (ITS 1)"
140..297
/gene="5.8S rRNA gene"
140..297
/gene="5.8S rRNA gene"
298..462
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misc_RNA 298..462
/note="Internal transcribed spacer 2 (ITS 2)"
463..>466
/gene="28S rRNA gene"
463..466
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BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tctagtacggtctgcgt 18
||||| |||||||

Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 10
NGA228665
LOCUS
DEFINITION NGA228665 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL
40782).

ACCESSION
VERSION AJ228665 GI:4210760
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.

SOURCE
ORGANISM Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
1 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
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/isolate="MUCL 40782"
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5. .139
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/gene="28S rRNA gene"

gene 463. .466
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BASE COUNT 107 a 142 c 111 g 106 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||

Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 11
NGA228666
LOCUS
DEFINITION NGA228666 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate IMI
378754).

ACCESSION
VERSION AJ228666 GI:4210761
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.

SOURCE
Neonectria galligena.

ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
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misc_RNA 5. .139
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RNA 140. .297
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140. .297
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gene 298. .462
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463. .>466
/gene="28S rRNA gene"

RNA 463. .466
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BASE COUNT 107 a 142 c 111 g 106 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||

Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 12
NGA228667
LOCUS
DEFINITION NGA228667 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL
40717).

ACCESSION
VERSION AJ228667 GI:4210762
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.

SOURCE
ORGANISM Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
1 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
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140..297
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140..297
/gene="5.8S rRNA gene"
238..462
/Note="Internal transcribed spacer 2 (ITS 2)"
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463..>466
/gene="28S rRNA gene"
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107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 13
NGA228668
LOCUS
DEFINITION
Nectria galligena Internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and Internal transcribed spacer 2 (ITS 2) (Isolate MUCL
40784).
ACCESSION
AJ228668
VERSION
AJ228668.1 GI:4210763
KEYWORDS
18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE
Neonectria galligena.
Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE
Langrell,S.R.H.
1 (bases 1 to 466)
Direct Submission
Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)
Langrell,S.R.H.
Unpublished
FEATURES
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140..297
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238..462
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/Note="Internal transcribed spacer 2 (ITS 2)"
463..>466

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/gene="28S rRNA gene"
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107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 14
NGA228669
LOCUS
DEFINITION
Nectria galligena Internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and Internal transcribed spacer 2 (ITS 2) (Isolate ICMP
13269).
ACCESSION
AJ228669
VERSION
AJ228669.1 GI:4210764
KEYWORDS
18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE
Neonectria galligena.
Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE
Langrell,S.R.H.
1 (bases 1 to 466)
Direct Submission
Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)
Langrell,S.R.H.
Unpublished
FEATURES
Location/Qualifiers
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140..297
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238..462
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107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

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Best Local Similarity 91.1%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

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RESULT 15
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LOCUS              Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
DEFINITION         gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS
                    100325).
ACCESSION          AJ228670.1  GI:4210765
VERSION            AJ228670
KEYWORDS            18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
                    5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
                    ITS1; ITS2.
SOURCE              Neonectria galligena.
ORGANISM            Neonectria galligena
                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                    Hypocerales; Nectriaceae; Neonectria.
REFERENCE           1 (bases 1 to 466)
AUTHORS             Langrell,S.R.H.
TITLE               Direct Submission
JOURNAL             Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
                    Sciences, Wye College, University of London, Wye, Ashford, Kent.,
                    TN25 5AH, UNITED KINGDOM
REFERENCE           2 (bases 1 to 466)
AUTHORS             Langrell,S.R.H.
JOURNAL             Unpublished
FEATURES             Location/Qualifiers
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                                     /gene="18S rRNA gene"
                                     /note="internal transcribed spacer 1 (ITS 1)"
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                                     107 a 142 c 111 g 106 t
BASE COUNT          107 a 142 c 111 g 106 t
ORIGIN

Query Match          91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. NO. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tctagtgcaggtctcgct 18
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Db 365 TCTAGTGCAGGCTCGCT 382

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Search completed: August 21, 2002, 22:09:50
 Job time: 14204 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:42 ; Search time 594.49 Seconds
(without alignments)
51.985 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtgacggctcgcgt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	20	AAV83696
2	16.4	91.1	310	20	AAV70851
3	16.4	91.1	502	21	AAV61893
4	16.4	91.1	2293	23	AAV16211
5	15.4	85.6	744	21	AAV42796
6	15	83.3	1182	19	AAV99142
7	15	83.3	1596	23	AAV88320
8	14.8	82.2	506	22	AAV08445
9	14.8	82.2	1502	22	AAV08412

10	14.4	80.0	51	22	AAV74530
11	14.4	80.0	51	22	AAV74531
12	14.4	80.0	945	22	AAV3958
13	14.4	80.0	1146	22	AAV3831
14	14.4	80.0	2982	22	AAV54021
15	14.4	80.0	3116	22	AAV54884
16	14.4	80.0	46899	15	AAV54386
17	14	77.8	479	22	AAV75543
18	14	77.8	479	22	AAV40157
19	14	77.8	479	22	AAV24114
20	14	77.8	479	22	AAV50175
21	14	77.8	479	22	AAV27255
22	14	77.8	479	22	AAV56113
23	14	77.8	489	22	AAV08494
24	14	77.8	550	22	AAV63091
25	14	77.8	550	22	AAV30343
26	14	77.8	550	22	AAV11513
27	14	77.8	550	22	AAV37292
28	14	77.8	550	22	AAV18119
29	14	77.8	550	22	AAV43123
30	14	77.8	615	15	AAV62632
31	14	77.8	636	17	AAV87815
32	14	77.8	639	16	AAV080291
33	14	77.8	642	20	AAV28805
34	14	77.8	645	16	AAV080293
35	14	77.8	649	21	AAV59451
36	14	77.8	666	15	AAV73443
37	14	77.8	666	17	AAV87817
38	14	77.8	699	22	AAV77315
39	14	77.8	717	16	AAV92504
40	14	77.8	735	16	AAV92500
41	14	77.8	735	16	AAV92502
42	14	77.8	777	17	AAV42507
43	14	77.8	780	21	AAV27848
44	14	77.8	798	13	AAV30706
45	14	77.8	798	15	AAV44642

ALIGNMENTS

RESULT 1	AAV83696	AAV83696 standard; DNA; 18 BP.
ID	AAV83696	
AC	AAV83696	
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DT	26-FEB-1999	(first entry)
XX		
DE	Species-specific probe targeted to the internal transcribed spacer 2.	
XX		
KW	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;	
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;	
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;	
KW	M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;	
KW	R. circinellus; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;	
KW	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;	
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.	
XX		
OS	Synthetic.	
OS	Fusarium moniliforme.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base 1	/*tag- 2
FT		/note- "labelled with digoxigenin"
PN	W09850584-A2.	
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PD	12-NOV-1998.	
XX		
PF	01-MAY-1998;	98WO-US08926.
XX		

Human silent SNP c
Human silent SNP c
S. epidermidis ope
S. epidermidis ope
S. epidermidis gen
S. epidermidis gen
T. niivum Cyclospo
Human foetal liver
Probe #18623 for g
Human brain expres
Human bone marrow
Probe #17188 for g
Probe #24799 used
Human Fc-gamma rec
Human foetal liver
Probe #8809 for ge
Human brain expres
Human bone marrow
Probe #8052 for ge
Probe #11809 used
Porphyria antibody
Antibody 7612 heav
Monoclonal antibod
Coding sequence fo
Monoclonal antibod
Antibody Fab fragm
6D9 antibody heavy
Antibody 3G2 heavy
19G Fab-BPI fusion
Mouse antibody H3-
Mouse antibody FB3
Murine antibody F4-
Murine A5B57 Fd fr
MOW-1 Fab heavy ch
Sequence of clone
Fd phage clone seq

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PR 02-MAY-1997; 97US-0045400.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX WPI: 1999-034737/03.
XX
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX species.
XX
XX Example 1: Page 22; 45pp; English.
XX
XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
XX (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
XX are species-specific, and can be used for identifying a species selected
XX from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
XX nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
XX plumbeus, M. indicus, M. circinellioide f. circinelloides, Rhizopus
XX oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor
XX pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
XX boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
XX Sporothrix schenckii. The probes can be used for differentiating
XX filamentous fungal species from each other and from other medically
XX important fungi.
XX
XX Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 18; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 tctagtgcggtctcgct 18
DB 1 tctagtgcggtctcgct 18
XX
XX
XX RESULT 2
XX ID AAV70851 standard; DNA; 310 BP.
XX
XX AAV70851;
XX
XX 26-FEB-1999 (first entry)
XX
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX
XX Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;
XX A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
XX Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
XX M. circinellioide f. circinelloides; Rhizopus oryzae; R. microsporus;
XX R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
XX Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
XX Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
XX Fusarium moniliforme.
XX
XX W09850584-A2.
XX
XX 12-NOV-1998.
XX
XX 01-MAY-1998; 98WO-US08926.
XX
XX 02-MAY-1997; 97US-0045400.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX WPI: 1999-034737/03.

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```

XX
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX species.
XX
XX Claim 1; Page 12; 45pp; English.
XX
XX The present sequence represents an internal transcribed spacer 2 (ITS2)
XX and adjacent regions. Probes can be derived from the present sequence
XX which are species-specific. The specification also describes ITS2
XX sequence-derived probes for identifying a species selected from
XX Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
XX Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
XX M. indicus, M. circinellioide f. circinelloides, Rhizopus oryzae,
XX R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
XX Absidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
XX (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
XX Sporothrix schenckii. The probes can be used for differentiating
XX filamentous fungal species from each other and from other medically
XX important fungi.
XX
XX Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 other;
XX
XX
XX Query Match 91.1%; Score 16.4; DB 20; Length 310;
XX Best Local Similarity 94.4%; Pred. No. 19;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 tctagtgcggtctcgct 18
DB 174 tctagtgcggtctcgct 191
XX
XX
XX RESULT 3
XX ID AAA61893 standard; DNA; 502 BP.
XX
XX AAA61893;
XX
XX 14-NOV-2000 (first entry)
XX
XX Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX
XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
XX HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
XX acquired immunodeficiency syndrome; AIDS; AIDS-related complex;
XX symptomatic infection; asymptomatic infection; potential HIV exposure;
XX combination therapy; ds.
XX
XX Fusarium sp. MF6381.
XX
XX W0200036132-A1.
XX
XX 22-JUN-2000.
XX
XX 09-DEC-1999; 99WO-US29356.
XX
XX 14-DEC-1998; 98US-0112168.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
XX Dombrowski AW;
XX WPI: 2000-431606/37.
XX
XX New steroid compounds are HIV integrase inhibitors used for treating
XX HIV infection and AIDS -
XX
XX Disclosure; Page 14; 113pp; English.
XX
XX The invention relates to novel steroid compounds derived from the

```

Query Match	Score	DB	Length
Best Local Similarity	91.1%	16.4	21
Matches	17	Conservative	0
		Mismatches	1
		Indels	0
		Gaps	0

PA	(LEEM/)	LEE M. D.
XX		
PI	Gallazzo JL,	Lee MD;
XX		
DR	WPI: 2001-662197/76.	
XX		
PT	A new method for producing a mixture of gibberellins from Gibberella	
PT	fujikuroi results in high titers of GA4 and GA7 useful to promote	
PT	flowering and fruit growth in the fruit growing industry	-
XX		
PS	Example 4: Column 9-12; 7pp; English.	
XX		
CC	This sequence represents a genomic DNA sequence containing the 18S rRNA	
CC	gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S	
CC	rRNA sequences from a mutant strain of Gibberella fujikuroi (LrB-1027)	
CC	of the invention. This region of DNA is highly variable and can be used	
CC	for species and strain differentiation. The LrB-1027 mutant produces a	
CC	mixture of gibberellins which is at least 70 % GA ₄ and GA ₇ .	
CC	Gibberellins GA ₄ and GA ₇ promote flowering and fruit cell elongation,	
CC	and are used by growers of apples, pears and grapes to produce larger	
CC	fruits and earlier harvests. The mixture of GA ₃ , GA ₄ and GA ₇ achieved	
CC	using the method of this invention should be particularly useful in the	
CC	apple industry where GA ₄ has been found more effective in russet	
CC	control and in promoting fruit set. This method produces GA ₄ and GA ₇	
CC	in much higher titers than prior art methods.	
XX		
SO	Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;	
	Query Match	51.1%; Score 16.4; DB 23; Length 2293;
	Best Local Similarity	94.4%; Pred. No. 22;
	Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 tctatgacgctcgcgt 18	
DB	2145 tctagtgcgctcgcgt 2162	
RESULT 5		
AAC42796		
ID	AAC42796 standard; DNA; 744 BP.	
AC	AAC42796;	
XX		
DT	17-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 36883.	
XX		
KM	Hybridisation assay: genetic mapping; gene expression control;	
KM	protein identification; signal transduction pathway;	
XX	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
PD		
XX	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
XX		
PR	25-FEB-1999; 99US-0121825.	
PR	05-MAR-1999; 99US-0123180.	
PR	09-MAR-1999; 99US-0123548.	
PR	23-MAR-1999; 99US-0125788.	
PR	23-MAR-1999; 99US-0126264.	
PR	29-MAR-1999; 99US-0126785.	
PR	01-APR-1999; 99US-0127462.	
PR	06-APR-1999; 99US-0128234.	
PR	08-APR-1999; 99US-0128714.	
PR	16-APR-1999; 99US-0128845.	
PR	19-APR-1999; 99US-0130077.	
PR	21-APR-1999; 99US-0130449.	
PR	23-APR-1999; 99US-0130510.	

PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140822.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143547.
PR 14-JUL-1999; 99US-0143622.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147392.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.

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PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

```

Query Match 85.6%; Score 15.4; DB 21; Length 744;
 Best Local Similarity 94.1%; Pred. No. 70;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 ctatgtacgctcgcct 18
   ||||| ||||| ||||| |||||
DB 218 ctatgtacgctcgcct 234

```

RESULT 6
 AAT99142/C
 ID AAT99142 standard; cDNA to mRNA; 1182 BP.

```

XX AC AAT99142;
XX DT 26-MAR-1998 (first entry)
XX DE S-adenosylmethionine synthase 2 gene.
XX KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
XX sam2; ss.
XX OS Hordeum vulgare.
XX PN JP09313186-A.
XX PD 09-DEC-1997.
XX PF 28-MAY-1996: 96JP-0133406.
XX PR 28-MAY-1996: 96JP-0133406.
XX PA (NIOC ) NIPPON OIL CO LTD.
XX DR WPI: 1998-080077/08.
XX DR P-PSDB; AAW34541.
XX PT S-adenosyl-methionine synthase gene - useful in producing plants
XX PT resistant to alkaline soil
XX PS Claim 5; Page 9-10; 13pp; Japanese.
XX CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)
CC CC gene. This DNA sequence may be used in a vector to produce plants which
CC CC are resistant to alkaline soil.
XX SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

```

Query Match 83.3%; Score 15; DB 19; Length 1182;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 taatgacgctcgc 17
   ||||| ||||| |||||
DB 145 TAGTACGCTCCG 131

```

RESULT 7
 AAS88320
 ID AAS88320 standard; cDNA; 1596 BP.

```

XX AC AAS88320;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #24124.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN W0200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB; ABG24133.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1; SEQ ID NO 24124; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations in
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1596 BP; 405 A; 350 C; 462 G; 379 T; 0 other;

```

Query Match 83.3%; Score 15; DB 23; Length 1596;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy      4 agtgcgctcgcct 18
          |||||
Db      1378 agtgcgctcgcct 1392

RESULT 8
AADD08445/C
ID      AADD08445 standard; cDNA; 506 BP.
XX
AC      AADD08445;
XX
DT      09-AUG-2001 (first entry)
XX
DE      Human secreted protein-encoding gene 9 cDNA clone HOVAF78, SEQ ID NO:52.
XX
KW      Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW      foetal abnormality; developmental abnormality; haematopoietic disorder;
KW      immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW      Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW      portalis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW      inflammation; neurological disorder; Alzheimer's disease; food additive;
KW      angiotensin-related disorder; kidney disorder; gastrointestinal disorder; allergy;
KW      pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW      cell culture; chemotaxis; vulnery; binding partner identification;
KW      gene therapy; chromosome 19; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      CDS
FT      269..505
FT      /*tag- a
FT      /product- "Human secreted protein precursor"
FT      /transl_except- (pos:311..313, aa:xaa)
FT      /transl_except- (pos:329..331, aa:xaa)
FT      /transl_except- (pos:413..415, aa:xaa)
FT      /transl_except- (pos:461..463, aa:xaa)
FT      /transl_except- (pos:464..466, aa:xaa)
FT      /note- "Xaa equals any of the naturally occurring
FT      L-amino acids; CDS does not include stop codon"
FT      /partial
FT      sig_peptide
FT      269..322
FT      /*tag- b
FT      mat_peptide
FT      323..505
FT      /*tag- c
FT      /product- "Mature human secreted protein"
XX
PN      WO200134643-A1.
XX
PD      17-MAY-2001.
XX
PF      08-NOV-2000; 2000MO-US30629.
XX
PR      12-NOV-1999; 99US-0164825.
PR      03-AUG-2000; 2000US-0222904.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
XX
DR      WPI: 2001-374441/39.
XX
DR      P-PSDB: AAE04140.
XX
PT      Nucleic acids encoding 24 human secreted polypeptides, useful for
PT      preventing, diagnosing and/or treating e.g. Gaucher's disease,
PT      Alzheimer's disease, Scitilar syndrome, Creutzfeldt-Jacob disease,
PT      diabetes mellitus and multiple sclerosis -
XX
PS      Claim 1: Page 445; 532pp; English.
XX
CC      AADD08404-AADD08478 represent cDNAs corresponding to 24 human secreted
CC      protein genes, and AAE004100-AAE004170 represent the proteins they encode.
CC      AAE04172-AAE04197 represent human secreted protein fragments or variants.
```

```
CC      The secreted proteins and their genes are useful for preventing, treating
CC      or ameliorating medical conditions, e.g., by protein or gene therapy.
CC      Pathological conditions can be diagnosed by determining the amount of the
CC      new protein in a sample or by determining the presence of mutations in
CC      the new genes. Specific uses are described for each of the 24 genes,
CC      based on the tissues in which they are most highly expressed, and include
CC      developing products for the diagnosis or treatment of proliferative
CC      disorders, cancer, tumours, foetal and developmental abnormalities,
CC      haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC      diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC      neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC      cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC      psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC      angiotensin disorders, kidney disorders, gastrointestinal disorders,
CC      pregnancy-related disorders, endocrine disorders, and infections. The
CC      proteins can also be used to aid wound healing and epithelial cell
CC      proliferation, to prevent skin aging due to sunburn, to maintain organs
CC      before transplantation, for supporting cell culture of primary tissues,
CC      to regenerate tissues, to identify their cognate ligands or binding
CC      partners, and in chemotaxis, and can be used as a food additive or
CC      preservative to modify storage properties. Antibodies specific for a
CC      protein of the invention can be used in alleviating symptoms associated
CC      with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC      radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC      The present sequence represents a human secreted protein-encoding cDNA of
CC      the invention.
XX
SQ      Sequence 506 BP, 134 A; 117 C; 122 G; 128 T; 5 other;
XX
Query Match      82.2%; Score 14.8; DB 22; Length 506;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      1 tctagtgcgctcgcct 18
          ||| ||| ||| ||| |||
Db      379 TCTGTTGAAGCTCTCGCT 362

RESULT 9
AADD08412/C
ID      AADD08412 standard; cDNA; 1502 BP.
XX
AC      AADD08412;
XX
DT      09-AUG-2001 (first entry)
XX
DE      Human secreted protein-encoding gene 9 cDNA clone HOVAF78, SEQ ID NO:19.
XX
KW      Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW      foetal abnormality; developmental abnormality; haematopoietic disorder;
KW      immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW      Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW      portalis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW      inflammation; neurological disorder; Alzheimer's disease; food additive;
KW      angiotensin-related disorder; kidney disorder; gastrointestinal disorder; allergy;
KW      pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW      cell culture; chemotaxis; vulnery; binding partner identification;
KW      gene therapy; chromosome 19; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      CDS
FT      269..481
FT      /*tag- a
FT      /product- "Human secreted protein precursor"
FT      /transl_except- (pos:311..313, aa:xaa)
FT      /transl_except- (pos:329..331, aa:xaa)
FT      /transl_except- (pos:413..415, aa:xaa)
FT      /transl_except- (pos:461..463, aa:xaa)
FT      /transl_except- (pos:464..466, aa:xaa)
FT      /note- "Xaa equals any of the naturally occurring
FT      L-amino acids; CDS does not include stop codon"
FT      /partial
FT      sig_peptide
FT      269..322
FT      /*tag- b
FT      mat_peptide
FT      323..478
FT      /*tag- c
FT      /product- "Mature human secreted protein"
XX
PN      WO200134643-A1.
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PD	17-MAY-2001.
XX	
XX	08-NOV-2000; 2000WO-US30629.
PF	
XX	12-NOV-1999; 99US-0164825.
PR	
XX	03-AUG-2000; 2000US-0222904.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
P1	Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
DR	WPI; 2001-374441/39.
XX	
XX	P-PSDB; AAEO4108.
PT	
PT	Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Sclimtar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis -
PS	
XX	Claim 1; Page 421-422; 532pp; English.
XX	
CC	AAED08404-AAED08478 represent cDNAs corresponding to 24 human secreted protein genes, and AAEO4100-AAEO4170 represent the proteins they encode. AAEO41172-AAEO4197 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiotonic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC	The present sequence represents a human secreted protein-encoding cDNA of the invention.
CC	
XX	
SO	Sequence 1502 BP: 377 A; 340 C; 338 G; 447 T; 0 other;
	Query Match 82.2%; Score 14.8; DB 22; Length 1502;
	Best Local Similarity 88.9%; Pred. No. 1.6e-02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY	1 tctagtgaacgctcgcgt 18
DB	379 TCTGCTGAAGCTCTCGCT 362
RESULT 10	
AAI74530	
ID	AAI74530 standard; DNA: 51 BP.
XX	
AC	AAI74530;
XX	
DT	09-NOV-2001 (first entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:1471.

[illegible]

XX	Homo sapiens.
PN	MO200140521-A2.
PD	07-JUN-2001.
PF	30-NOV-2000; 2000WO-US32758.
PR	30-NOV-1999; 99US-0168138.
PR	29-NOV-2000; 2000US-0726173.
PA	(CURA-) CURAGEN CORP.
PI	Shimkets RA, Leach M;
DR	WPI: 2001-356160/37.
PT	Polyomorphic nucleic acid sequences, useful in genetic testing and therapy -
PS	Claim 1: Page 504; 2653pp; English.
XX	AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC	AAM53114 to AAH53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein CC
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression of polymorphic polypeptides. CC
CC	For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of CC
CC	polypeptides by expressing inactive proteins or to supplement the CC patients own production of polypeptide. Additionally, (I) and its CC complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids CC
CC	in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the CC production of antibodies specific for polymorphic polypeptides. The CC
CC	antibodies may also be used to down regulate expression and activity. CC
CC	The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.
XX	
SQ	Sequence 51 BP: 22 A; 11 C; 11 G; 7 T; 0 other;
OY	Query Match 80.0%; Score 14.4; DB 22; Length 51; Best Local Similarity 93.8%; Pred. No. 1.9e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0. 1 tctagtgcaggtctcg 16 29 tctagtgaagttctg 44
ID	AAH53958/c
AC	AAH53958 standard; DNA; 945 BP.
DT	03-SEP-2001 (first entry)
DE	5. epidermidis open reading frame nucleotide sequence SEQ ID NO:3309.
KM	Staphylococcus epidermidis SRI strain; infection; diagnosis;
OS	Staphylococcus epidermidis.
PN	MO200134809-A2.
PD	17-MAY-2001.

XX	Pf	09-NOV-2000; 2000MO-US30782.
XX	PR	09-NOV-1999; 99US-0164258.
XX	PA	(GLAX) GLAXO GROUP LTD.
XX	PI	Kimmerly WJ;
XX	DR	WPI: 2001-316495/33.
XX	DR	P-PsDB; AAG83108.
PT	Nucleic acids encoding polypeptides from Staphylococcus epidermidis,	
PT	useful for vaccinating against infections, e.g. endocarditis -	
XX	Claim 8: Page 872: 2188pp: English.	
CC	AH52304 to AH53970 represent nucleic acids (I) encoding polypeptides	
CC	((I)), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.	
CC	(I) and ((I)) can have antibacterial activity and therefore can be used	
CC	in vaccination. The nucleic acids (I) may be used to produce the	
CC	S. epidermidis polypeptides ((I)) via the production of vectors	
CC	containing them which are used to produce hosts cells which express the	
CC	polypeptides. The polypeptides ((I)) (and/or nucleic acids) may then be	
CC	used to vaccinate subjects and to raise antibodies against the bacteria.	
CC	The polypeptides may also be used to assay for other inhibitors of their	
CC	activity and therefore identify compounds that may be used for the	
CC	treatment of S. epidermidis infections, e.g. endocarditis. AH53971 to	
CC	AH55090 represent specifically claimed S. epidermidis genomic DNA	
CC	polynucleotide sequences from the present invention. AH55091 to	
CC	AH55098 represent oligonucleotide sequences and primers which are used	
CC	N.B. The present invention specifically claims all the polynucleotide	
CC	sequences given in the sequence listing of the present specification,	
CC	however the sequence listing only goes up to SEQ ID NO:4454 so even	
CC	though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,	
CC	no sequences are present for SEQ ID NO:4455 to 4464.	
XX	Sequence 945 BP; 356 A; 139 C; 201 G; 249 T; 0 other;	
QY	Query Match 80.0%; Score 14.4; DB 22; Length 945;	
	Best Local Similarity 93.8%; Pred. No. 2.5e+02;	
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Db	268 CTACTGACGGCTCGC 253	
XX	AAH53831/C	
ID	AAH53831 standard; DNA; 1146 BP.	
XX	AAH53831:	
DT	03-SEP-2001 (first entry)	
DE	S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3055.	
KM	Staphylococcus epidermidis SRI strain; infection; diagnosis;	
RN	vaccination; endocarditis; ds.	
OS	Staphylococcus epidermidis.	
PN	MO200134809-A2.	
PD	17-MAY-2001.	
Pf	09-NOV-2000; 2000MO-US30782.	
PR	09-NOV-1999; 99US-0164258.	
PA	(GLAX) GLAXO GROUP LTD.	

XX kimerly wj;
PI WPI; 2001-316495/33.
DR P-PSDB; AAG82981.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PS useful for vaccinating against infections, e.g. endocarditis -
PS Claim 8; Page 804; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 1146 BP; 437 A; 168 C; 230 G; 311 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 1146;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctatgacggtctcgc 17
||| |||||
DB 469 CTACTGACGCTCCG 454

RESULT 14
AAH54021
ID AAH54021 standard; DNA: 2982 BP.
XX
AC AAH54021;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3385.
XX
KW Staphylococcus epidermidis SRI strain; Infection; diagnosis;
KM vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimerly wj;
XX
PS WPI; 2001-316495/33.
XX

PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
PS Claim 8; Page 938-939; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 2982 BP; 753 A; 592 C; 434 G; 1203 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 2982;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctatgacggtctcgc 17
||| |||||
DB 1311 ctactgacggtctcgc 1326

RESULT 15
AAH54884
ID AAH54884 standard; DNA: 3116 BP.
XX
AC AAH54884;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4248.
XX
KW Staphylococcus epidermidis SRI strain; Infection; diagnosis;
KM vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimerly wj;
XX
PS WPI; 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
PS Claim 8; Page 1970-1971; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

CC (11), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (1) and (11) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC *S. epidermidis* polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (11) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed *S. epidermidis* genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to
CC AAH5098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX

Sequence 3116 BP; 966 A; 578 C; 454 G; 1118 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 3116;
Best Local Similarly 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctatgacggtctcgc 17
||| |||||
Db 1615 ctactgacggtctcgc 1630

Search completed: August 21, 2002, 22:22:44
Job time: 5784 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:13 ; Search time 5019.06 Seconds

(without alignments)
48.405 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtgcgcgtcgcgt 18

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estdb:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_hlc:*
13: em_gss_hum:*
14: em_gss_lin:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	936	12	CNS03M43
2	15.4	85.6	481	12	BH625357
3	15.4	85.6	486	10	BE784335
4	15.4	85.6	626	10	BJ130132
5	15.4	85.6	629	10	BJ147480
6	15.4	85.6	703	9	AU004847
7	15.4	85.6	718	9	AV398645
8	15.4	85.6	1005	10	BG760845
9	15.4	85.6	1311	10	BG757034
10	15.4	83.3	112	9	AV940706
11	15.4	83.3	168	9	AV922948
12	15.4	83.3	241	9	AA324668
13	15.4	83.3	256	9	AA367189
14	15.4	83.3	276	9	AA339193
15	15.4	83.3	329	9	AA351943
16	15.4	83.3	360	12	TA301E06P
17	15.4	83.3	362	10	N49663

18	83.3	369	10	BF438464
19	83.3	370	9	AA324673
20	83.3	375	9	AL134474
21	83.3	398	10	H20232
22	83.3	400	10	BG119356
23	83.3	406	9	AI347337
24	83.3	411	9	AV939224
25	83.3	427	10	BI461101
26	83.3	430	10	BE438640
27	83.3	442	10	BE868742
28	83.3	445	10	BM377636
29	83.3	447	10	BM369940
30	83.3	460	10	BI756944
31	83.3	462	10	BF038758
32	83.3	466	10	BE262001
33	83.3	469	12	AO685141
34	83.3	470	10	W05422
35	83.3	478	10	BI334225
36	83.3	484	10	BE513967
37	83.3	488	10	BG700095
38	83.3	490	10	BI836611
39	83.3	493	10	BG424777
40	83.3	493	10	BF630275
41	83.3	495	10	BG707736
42	83.3	503	10	BI771378
43	83.3	505	10	BI818791
44	83.3	505	9	AM672790
45	83.3	506	9	AA182515

ALIGNMENTS

RESULT 1	CNS03M43	936 bp	DNA	linear	GSS 17-MAY-2000
LOCUS	Tetraodon nigroviridis genome survey sequence T7 end of clone				
DEFINITION	037103 of library G from Tetraodon nigroviridis, genomic survey				
ACCESSION	AL250284				
VERSION	AL250284.1 GI:7971296				
KEYWORDS	GSS: genome survey sequence.				
SOURCE	Tetraodon nigroviridis.				
ORGANISM	Tetraodon nigroviridis				
REFERENCE	Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei: Acanthomorphi: Acanthopterygii: Percomorphi: Tetraodontiformes: Tetraodontidae: Tetraodon.				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and Weissenbach,U.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
JOURNAL	Unpublished				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Quetler,F., Saurin,W. and Weissenbach,U.				
REFERENCE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
AUTHORS	Unpublished				
REFERENCE	3 (bases 1 to 936)				
AUTHORS	Genoscope.				
TITLE	Direct Submision				
COMMENT	Submitted (12-Apr-2000) to the EMBL/Genbank/DBJ databases				
FEATURES	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at				
source	http://www.genoscope.cns.fr/tetraodon.				
	Location/Qualifiers				
	1..936				
	/organism="Tetraodon nigroviridis"				

/db_xref="taxon:99883"
 /clone="037103"
 /clone_11b="G"
 /note="Genoscope sequence ID : C0B6037AE02LP1-end : 77"
 BASE COUNT 174 a 259 c 267 g 236 t
 ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 936;
 Best Local Similarity 94.4%; Pred. No. 4.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctatgtacggtctcgcct 18
 |||
 Db 168 TCCAGTGACGCTCGCT 185

RESULT 2
 BH625357 481 bp DNA linear GSS 30-JAN-2002
 LOCUS 1007106H02.y1 1007 - Rescuemu Grid H zea mays genomic, DNA
 DEFINITION sequence.
 ACCESSION BH625357 GI:18438608
 VERSION BH625357
 KEYWORDS GSS.
 SOURCE zea mays.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 481)
 Walbot,V.
 Maize genomic sequences found using engineered Rescuemu transposon
 Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1007106 column: 29
 Class: transposon-tagged.
 Location/Qualifiers
 1..481
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_11b="1007 - Rescuemu Grid H"
 /tissue-type="leaf"
 /dev-stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescuemu (engineered from
 Bluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescuemu, go to the web
 site 'www.zmmb.iastate.edu' and follow the links for
 'Rescuemu.' Grid H was grown at Berkeley in 2001. DNA
 was extracted from leaf punches, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

BASE COUNT 68 a 193 c 127 g 93 t
 ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 481;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctatgtacggtctcgcct 18
 |||
 Db 410 CTAGTGACGCGCTCGCT 394

RESULT 3
 BE784335 486 bp mRNA linear EST 20-OCT-2000
 LOCUS 601473488F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876716 5',
 mRNA sequence.
 ACCESSION BE784335
 VERSION BE784335.1 GI:10205533
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 486)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM637 row: 0 column: 21
 High quality sequence stop: 160.
 Location/Qualifiers
 1..486
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3876716"
 /clone_11b="NIH_MGC_68"
 /tissue-type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: PCMV-SpORF6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

BASE COUNT 196 a 100 c 92 g 98 t
 ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 486;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctatgtacggtctcgcct 18
 |||
 Db 232 CAACTGACGCTCGCT 216

RESULT 4
 B1130132 626 bp mRNA linear EST 23-JAN-2002
 LOCUS B1130132 unpublished oligo-capped cDNA library, C. elegans L1 stage
 DEFINITION Caenorhabditis elegans cDNA clone yk1039d08 3', mRNA sequence.
 ACCESSION B1130132
 VERSION B1130132.1 GI:18290289
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea
 ; Rhabditidae; Peloiderinae; Caenorhabditis.
 1 (bases 1 to 626)
 Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
 and Sugano,S.

REFERENCE
 AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
 and Sugano,S.

TITLE A complementary view of the *C. elegans* genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 626
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1039d08"
/clone_1lb="unpublished oligo-capped cDNA library, C. elegans L1 stage"
/sex="hermaphrodite"
/tissue.type="whole animal"
/dev_stage="L1"
/dev_stage="L1"

BASE COUNT 151 a 145 c 135 g 190 t 5 others
ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 626;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctagtgcaggtctgcgt 18
||| ||||| ||||| |||||
Db 455 TCNAGTGACGGCTCGCT 472

RESULT 5
BJ147480 629 bp mRNA linear EST 24-JAN-2002
LOCUS BJ147480 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1251f07 3', mRNA sequence.
ACCESSION BJ147480
VERSION BJ147480.1 GI:18315465
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitae; Rhabdilitoidae
; Rhabdilitidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 629)
Kohara, Y., Shin, I., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the *C. elegans* genome
Unpublished (2002)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 629
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1251f07"
/clone_1lb="unpublished oligo-capped cDNA library, C. elegans L1 stage"
/sex="hermaphrodite"
/tissue.type="whole animal"
/dev_stage="L1"
/dev_stage="L1"

BASE COUNT 151 a 146 c 133 g 192 t 7 others
ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 629;

Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctagtgcaggtctgcgt 18
||| ||||| ||||| |||||
Db 456 TCNAGTGACGGCTCGCT 473

RESULT 6
AU004847/c 703 bp mRNA linear EST 19-JAN-1999
LOCUS AU004847 Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws20913,
DEFINITION mRNA sequence.
ACCESSION AU004847
VERSION AU004847.1 GI:4162218
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 703)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Establishment of cDNA database of Bombyx mori
Unpublished (1999)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmitsueni@rs.ri.go.jp.
PROJECT = 'CREST project by JST'.
Location/Qualifiers

FEATURES
source
1. 703
/organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws20913"
/clone_1lb="Bombyx mori p50(Daizo)"

BASE COUNT 182 a 142 c 145 g 234 t
ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 703;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgcaggtctgcgt 17
||| ||||| ||||| |||||
Db 491 TCTACTGACGGCTCTAGC 475

RESULT 7
AV398645/c 718 bp mRNA linear EST 05-FEB-2000
LOCUS AV398645 Bombyx mori ovary bmnPV infected: 6 hr after inoculation
DEFINITION Bombyx mori cDNA clone NV060125 T3, mRNA sequence.
ACCESSION AV398645
VERSION AV398645.1 GI:6902297
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 718)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmitsueni@rs.ri.go.jp

method:uni-directional, sequence direction:sequenced from 73 primer
(5' -> 3')
Project="Silkworm Genome Program in MAFF, and Research for the
Future Program in JSPS", see 'Silkbase',
<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1..718
/organism="Bombyx mori"
/db_xref="taxon:7091"
/clone_1lb="NV060125"
/clone_1lb="Bombyx mori ovary BmNPV infected; 6 hr after
inoculation"
/tissue_type="ovary"
/cell_type="BmNPV infected; 6 hr after inoculation"
/dev_stage="BmNPV infected; 6 hr after inoculation"

BASE COUNT

180 a 148 c 156 g 225 t 9 others

ORIGIN

Query Match 85.6% Score 15.4; DB 9; Length 718;
Best Local Similarity 94.1% Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtagcagctcgcg 17
|||||

Db 510 TCTAGTAGCAGCTCTAGC 494

RESULT 8

BC760845 1005 bp mRNA linear EST 15-MAY-2001
LOCUS 602717012F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840730 5',
DEFINITION mRNA sequence.

ACCESSION BC760845
VERSION EG760845.1 GI:14071485
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1005)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCDF/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM1672 row: g column: 03

High quality sequence stop: 90.

FEATURES

source

1..1005
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1IMAGE:4840730"

/clone_1lb="NIH_MGC_49"

/tissue_type="melanotic melanoma, high MDR (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

Query Match 85.6% Score 15.4; DB 10; Length 1005;
Best Local Similarity 94.1% Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ctatagtagcagctcgcg 18
|||||

Db 504 CTATAGTAGCAGCTCGCT 520

RESULT 9

BC757034 1311 bp mRNA linear EST 15-MAY-2001
LOCUS 602710452F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850749 5',
DEFINITION mRNA sequence.

ACCESSION BC757034
VERSION BG757034.1 GI:14067687
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1311)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM1692 row: h column: 14.

FEATURES

source

1..1311
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1IMAGE:4850749"

/clone_1lb="NIH_MGC_48"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pORF7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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BASE COUNT

231 a 245 c 385 g 144 t

RESULT 10

AV940706 112 bp mRNA linear EST 18-JAN-2002
LOCUS AV940706/c
DEFINITION AV940706 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum

Query Match 85.6% Score 15.4; DB 10; Length 1311;

Best Local Similarity 94.1% Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ctatagtagcagctcgcg 18
|||||

Db 222 CGAGTAGCAGCTCGCT 206

RESULT 10

AV940706 112 bp mRNA linear EST 18-JAN-2002
LOCUS AV940706/c
DEFINITION AV940706 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum

```

ACCESSION      AV940706      CDNA clone bah28115 5', mRNA sequence.
VERSION         AV940706.1    GI:18236503
KEYWORDS        Hordeum vulgare subsp. spontaneum.
SOURCE          EST.
ORGANISM        Hordeum vulgare subsp. spontaneum.
                Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
                ; Triticeae; Hordeum.
REFERENCE       1 (bases 1 to 112)
AUTHORS         Sato,K., Saisyo,D. and Takeda,K.
TITLE           Barley EST sequencing project in NIG and Okayama Univ
JOURNAL         Unpublished (2002)
COMMENT         Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshin@genes.nig.ac.jp.

FEATURES
  source
    1..112
    /organism="Hordeum vulgare subsp. spontaneum"
    /strain="H602"
    /db_xref="taxon:77009"
    /clone="bah28115"
    /clone_lib="K. Sato unpublished cDNA library, strain H602
    adult, heading stage top three leaves"
    /tissue_type="top three leaves"
    /dev_stage="adult, heading stage"
    25 a 34 c 32 g 20 t 1 others

BASE COUNT
  25 a 34 c 32 g 20 t 1 others

Query Match
  Best Local Similarity 100.0%; Pred. No. 1.1e+03;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 tagtgacggtctcgc 17
    |||
    67 TACTGACGCTCTCGC 53

RESULT 11
AV922948      168 bp      mRNA      linear      EST 18-JAN-2002
LOCUS         AV922948 K. Sato unpublished cDNA library, cv. Haruna Nijo second
DEFINITION    leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA
clone basd3b11 5', mRNA sequence.
ACCESSION     AV922948
VERSION       AV922948.1    GI:18218727
KEYWORDS      EST.
SOURCE        Hordeum vulgare subsp. vulgare.
ORGANISM      Hordeum vulgare subsp. vulgare
                Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
                ; Triticeae; Hordeum.
                1 (bases 1 to 168)
REFERENCE     1 (bases 1 to 168)
AUTHORS       Sato,K., Saisyo,D. and Takeda,K.
TITLE         Barley EST sequencing project in NIG and Okayama Univ
JOURNAL       Unpublished (2002)
COMMENT       Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshin@genes.nig.ac.jp.

FEATURES
  source
    1..168
    /organism="Hordeum vulgare subsp. vulgare"
    /cultivar="Haruna Nijo"
    /db_xref="taxon:112509"

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```

BASE COUNT      36 a 56 c 49 g 27 t

Query Match
  Best Local Similarity 100.0%; Pred. No. 1.3e+03;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 tagtgacggtctcgc 17
    |||
    111 TAGTGACGCTCTCGC 97

RESULT 12
AA324668      241 bp      mRNA      linear      EST 20-APR-1997
LOCUS         AA324668 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.
DEFINITION    AA324668
ACCESSION     AA324668.1    GI:1977158
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                1 (bases 1 to 241)
REFERENCE     Adams,M.D., Kerlavang,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
                C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
                O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
                Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
                L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodex,A.,
                Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
                Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
                Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
                Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
                Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
                Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
                Dimke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,W.M.,
                Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
                Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
                Wei,T.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
                M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
                Venter,J.C.
                Initial assessment of human gene diversity and expression patterns
                based upon 83 million nucleotides of cDNA sequence
                Nature 377 (6547 suppl), 3-174 (1995)
                96026280
                Other_ESTs: THCI90996
                Contact: Kerlavang, AR
                Bioinformatics
                The Institute for Genomic Research
                9712 Medical Center Drive, Rockville, MD 20850 USA
                Tel: 3018699056
                Fax: 3018699423
                Email: arkerlav@tigr.org
                For clone availability, additional sequence and expression
                information related to this EST, please check the TIGR Human Gene
                Index (http://www.tigr.org/tdb/hgi/hgi.html)
                Seq primer: M13 Reverse.

FEATURES
  source
    1..241
    /organism="Homo sapiens"
    /db_xref="ATCC (lnhost):125407"
    /db_xref="taxon:9606"
    /clone_lib="Cerebellum II"
    /tissue_type="cerebellum"
    /dev_stage="adult"
    /note="Organ: brain; Vector: pBluescript SK-; Site_1:
    EcoRI; Site_2: XhoI"

```


Db 188 AGTGACGCTCCT 174

RESULT 15

AM351943 329 bp mRNA linear EST 01-FEB-2000
LOCUS IL5-HT0009-180999-001-D12 HT0009 Homo sapiens cDNA, mRNA sequence.

AM351943
ACCESSION
VERSION AM351943.1 GI:6849656

KEYWORDS
EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 329)
HCCP <http://www.ludwig.org.br/ORESTES>.

AUTHORS
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?IL5&IL2=IL5-HT0009-180999-001-D12&IL3=1999-09-18&IL4=1>)

Seq primer: puc 18 forward
High quality sequence stop: 329.

FEATURES

Source

1..329
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0009"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 53 a 91 c 95 g 90 t
ORIGIN

Query Match 83.3%; Score 15; DB 9; Length 329;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 4 agtgacgctcgcct 18
|||||

Db 312 AGTGACGCTCCT 326

Search completed: August 21, 2002, 21:32:20
Job time: 12519 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:12:26 : Search time 138.45 Seconds
(without alignments)
31.935 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtgcgctcgcgt 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

767066

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/lna/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/lna/PCtUS_COMB.seq.*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	16.4	91.1	583	1	US-08-652-127C-8
2	16.4	91.1	594	1	US-08-652-127C-5
3	16.4	91.1	2293	4	US-09-645-073-1
4	14.8	82.2	531	1	US-08-652-127C-7
5	14.8	82.2	581	1	US-08-652-127C-6
6	14.4	80.0	46899	1	US-08-471-119A-1
7	14	77.8	636	2	US-08-737-129A-1
8	14	77.8	666	2	US-08-737-129A-5
9	14	77.8	717	5	PCT-US94-14106-58
10	14	77.8	735	5	PCT-US94-14106-54
11	14	77.8	735	5	PCT-US94-14106-54
12	14	77.8	777	2	US-08-860-862A-25
13	14	77.8	798	1	US-08-133-011-99
14	14	77.8	798	1	US-08-322-730A-99
15	14	77.8	798	1	US-08-387-874-71
16	14	77.8	798	2	US-08-383-619-99
17	14	77.8	798	4	US-08-907-739-99
18	14	77.8	798	5	PCT-US93-08364-71
19	14	77.8	830	1	US-08-133-011-115
20	14	77.8	830	1	US-08-322-730A-115
21	14	77.8	830	1	US-08-387-874-88
22	14	77.8	830	4	US-08-383-619-115
23	14	77.8	830	2	US-08-907-739-115
24	14	77.8	830	5	PCT-US93-08364-88
25	14	77.8	923	5	PCT-US94-07659-1
26	14	77.8	1347	6	5455030-2
27	14	77.8	1443	2	US-08-403-853-19

C 28	14	77.8	1446	4	US-09-171-945-130	Sequence 130, App
C 29	14	77.8	1572	1	US-08-353-400-23	Sequence 23, App1
C 30	14	77.8	1632	2	US-08-792-824-8	Sequence 8, App1
C 31	14	77.8	1641	2	US-08-792-824-5	Sequence 5, App1
C 32	14	77.8	1672	2	US-08-792-824-2	Sequence 2, App1
C 33	14	77.8	1797	1	US-08-442-542-17	Sequence 17, App1
C 34	14	77.8	1797	3	US-08-765-468-17	Sequence 17, App1
C 35	14	77.8	1800	2	US-08-579-940-6	Sequence 6, App1
C 36	14	77.8	1974	4	US-09-423-439-59	Sequence 59, App1
C 37	14	77.8	3343	6	5453363-2	Patent No. 5453363
C 38	14	77.8	4435	2	US-08-792-824-1	Sequence 360, App
C 39	13.8	76.7	431	4	US-09-439-313-360	Sequence 309, App
C 40	13.8	76.7	460	4	US-09-439-313-309	Sequence 22, App1
C 41	13.8	76.7	884	4	US-09-235-451-22	Sequence 10, App1
C 42	13.8	76.7	1270	1	US-08-247-907A-10	Sequence 10, App1
C 43	13.8	76.7	1270	4	US-08-452-772-10	Sequence 10, App1
C 44	13.8	76.7	1270	1	US-09-414-234-10	Sequence 10, App1
C 45	13.8	76.7	1270	5	PCT-US94-05288-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-08-652-127C-8
Sequence 8, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hameljin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 583
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-8

Query Match 91.1%; Score 16.4; DB 1; Length 583;
Best Local Similarity 94.4%; Pred. No. 3.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tctagtgcgctcgcgt 18
Db 429 tctagtgcgctcgcgt 446

```
RESULT 2
US-08-652-127C-5
; Sequence 5, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652.127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-652-127C-5
;
Query Match 91.1%; Score 16.4; DB 1; Length 594;
Best Local Similarity 94.4%; Pred. No. 3.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 tctagtgaaggtctgcgt 18
Db 439 TCTAGTGGCGCTCTCGCT 456

RESULT 3
US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titters of Glibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Glibberella fujiikuroi
US-09-645-073-1
;
Query Match 91.1%; Score 16.4; DB 4; Length 2293;
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Best Local Similarity 94.4%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 tctagtgaaggtctgcgt 18
Db 2145 tctagtgcggtctgcgt 2162

RESULT 4
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652.127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-652-127C-7
;
Query Match 82.2%; Score 14.8; DB 1; Length 531;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tctagtgaaggtctgcgt 18
Db 377 TATAGTGGCGCTCTCGCT 394

RESULT 5
US-08-652-127C-6
; Sequence 6, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 18:13:06 ; Search time 2238.68 Seconds
(without alignments)
3411.915 Million cell updates/sec

Title: US-10-046-955-5

Perfect score: 365
Sequence: 1 aaacttcaacaatgatct.....gggatacccgctgaacttaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*
2: gb_htg:*
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14: gb_vl:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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25: em_pl:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	365	100.0	365	8	EN093686	U93686 Emericella
2	334.8	91.7	560	8	EQ0000934	A0000934 Emericella
3	334.8	91.7	565	8	AF138289	AF138289 Emericella
4	327.6	89.8	561	8	EQ0000935	A0000935 Emericella
5	322.8	88.4	558	8	EQ0000931	A0000931 Emericella
6	318.8	87.3	496	8	EN1276063	AJ276063 Emericella
7	316.4	86.7	563	8	EV0000932	AJ0000932 Emericella
8	306.4	83.9	569	8	AF157507	AF157507 Aspergillus
9	304	83.3	549	8	AF261558	AF261558 Aspergillus
10	297.2	81.4	493	8	AF078899	AF078899 Emericella
11	295.6	81.0	493	8	AF078898	AF078898 Emericella
12	290.8	79.7	1148	8	AF033428	AF033428 Penicillium
13	288	78.9	581	8	AE065310	U65310 Aspergillus
14	286.8	78.6	1110	8	AF033421	AF033422 Penicillium
15	286.8	78.6	1110	8	AF033423	AF033423 Penicillium
16	286.8	78.6	1110	8	AF033425	AJ000936 Emericella
17	285.4	78.2	566	8	EJ0000936	AF033405 Penicillium
18	285.2	78.1	1144	8	AF033405	U93685 Aspergillus
19	284.2	77.9	365	8	AN093685	AF033433 Penicillium
20	283.2	77.6	1144	8	AF033433	AF033457 Penicillium
21	282.8	77.5	1141	8	AF033457	AJ280009 Aspergillus
22	281.6	77.2	579	8	AF0280009	AF033425 Eupenicillium
23	281.4	77.1	1147	8	AF033425	AJ223852 Aspergillus
24	281	77.0	595	8	ANA3852	U65304 Aspergillus
25	280.6	76.9	1150	8	AH065304	AF138288 Aspergillus
26	279.8	76.7	596	8	AF138288	AF348420 Aspergillus
27	279.8	76.7	614	8	AF348420	AJ280013 Aspergillus
28	279	76.4	600	8	AHE280013	AF033441 Penicillium
29	278.4	76.3	1142	8	AF033441	AF078889 Aspergillus
30	278.2	76.2	597	8	AF078889	AF459733 Neosartoris
31	278.2	76.2	1189	8	AF459733	AF033492 Penicillium
32	278	76.2	1141	8	AF033492	AF033402 Penicillium
33	278	76.2	1143	8	AF033402	AF033434 Penicillium
34	277.6	76.1	1145	8	AF033434	AF033416 Penicillium
35	276.8	75.8	1144	8	AF033416	AF033427 Penicillium
36	276.8	75.8	1144	8	AF033427	AF125946 Penicillium
37	276.8	75.8	1144	8	AF125946	AF125937 Penicillium
38	276.4	75.7	1141	8	AF125937	AF048741 Verticillium
39	276.2	75.7	566	8	AF048741	AF033415 Penicillium
40	275.8	75.6	1144	8	AF033415	AF034462 Penicillium
41	275.8	75.6	1144	8	AF034462	AF033429 Penicillium
42	275.8	75.6	1150	8	AF033429	AF033419 Penicillium
43	275.6	75.5	1143	8	AF033419	AF033417 Penicillium
44	275.6	75.5	1144	8	AF033417	AF034463 Penicillium
45	275.6	75.5	1141	8	AF034463	

ALIGNMENTS

RESULT 1

EN093686 365 bp DNA linear PLN 05-MAY-1997

LOCUS Emericella nidulans 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.

DEFINITION U93686

ACCESSION U93686.1 GI:2072177

VERSION U93686

KEYWORDS Emericella nidulans.

SOURCE Emericella nidulans

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.

REFERENCE 1 (bases 1 to 365)

AUTHORS De Aguiar, U.A., Vaisnav, H., Westernman, J.M., Reiss, E., Lotz, T.J. and Mortison, C.J.

TITLE Direct Submission

JOURNAL Submitted (28-FEB-1997) Mycology, Centers for Disease Control and Prevention, 1600 Clifton Road, N.E., Atlanta, GA 30333, USA

FEATURES

location/Qualifiers

1..365

/organism="Emericella nidulans"

/db_xref="taxon:162425"

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/note="CDC Mycological Reference Laboratory B5446"
rRNA
<1..157
/product="5.8S ribosomal RNA"
misc_RNA
158..327
/note="Internal transcribed spacer 2; ITS2"
rRNA
328..>365
/product="28S ribosomal RNA"
BASE COUNT      68 a      109 c      109 g      79 t
ORIGIN

Query Match      100.0%; Score 365; DB 8; Length 365;
Best Local Similarity 100.0%; Pred. No. 7, 8e-71;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 aaacttcaacaatgagatccttggtccgagcatgaaagaaagcagcgaactgcgat 60
        |||||||
        1 AAACCTTCAACAATGAGATCTTGTTCCGATCGATGAGAAGACGACGCACTGCGAT 60
DB
OY      61 aagtaatgtaattgcaagaatcagatcatcgaagtccttgaagcacatlgcggccc 120
        |||||||
        61 AAGTAATGTGAATTCACAATTCAGTGAATCATGAGCTTTGAAACGCACATTCGCGCCC 120
DB
OY      121 ctggcatccgaggggagcctgctcgcagagcgtcattgctgcccacaagcccgctgtg 180
        |||||||
        121 CTGGCATTCGGGGGGGAGCTGCTGTCAGAGGCTCATTCCTCCCAAGCCCGGCTTGTG 180
DB
OY      181 tgttggtcgtcgtcccccgcgggggagcggccgaaagcagcgcgccgctgc 240
        |||||||
        181 TGTTCGCTCCTGCTCCCGCCCGCGGGGACGGGCCAAAGGACGCGCGCACCGCTC 240
DB
OY      241 cggctcgcagcgtatggtggttgcacccgctcgaatgaagccggcgccgagcc 300
        |||||||
        241 CGGCTCGCAGCGATGAGGGGCTTGCTGTCACCCGCTGATTAAGCCGCGGCGCCACGCC 300
DB
OY      301 ggcgtcccaacctatcttctcaggttcagctcgcagtcagtaggatacccgctgaa 360
        |||||||
        301 GCGCTCCCAACCTTATCTTCTCAGTTGACCTCGATCGATGAGGATACCGCTGAA 360
DB
OY      361 cttaa 365
        |||||
        361 CTTAA 365
DB

RESULT 2
EOJ000934      560 bp      DNA      linear      PLN 12-OCT-1998
LOCUS      Emericella quadrillinea strain FMR 5966, 5.8S rRNA gene, ITS1 and
DEFINITION      ITS2.
ACCESSION      AJ000934
VERSION      AJ000934.1 GI:3757579
KEYWORDS      5.8S rRNA gene; ITS1; ITS2.
SOURCE      Emericella quadrillinea.
ORGANISM      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
        Eurotiales; Trichocomaceae; Emericella.
REFERENCE      Cano,J.F.
AUTHORS      Direct Submission
TITLE      Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA,
        FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç
        21, Reus, 43201 - Reus - Tarragona, SPAIN
REFERENCE      2 (bases 1 to 560)
AUTHORS      Schigel,A., Cano,J. and Guarco,J.
TITLE      A new species of Emericella and anomalous strains of
        E.quadrillinea
JOURNAL      Unpublished
FEATURES
        source      Location/Qualifiers
        1..560
        /organism="Emericella quadrillinea"
        /variety="gemmata"
        /strain="FMR 5966"
        /db_xref="taxon:41735"
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/tissue_type="mycelium/hyphal"
misc_feature
30..182
/note="Internal transcribed spacer 1 (ITS1)"
rRNA
183..339
/gene="5.8S rRNA"
/citation=[2]
/product="5.8S ribosomal RNA"
gene
183..339
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misc_feature
340..560
/note="Internal transcribed spacer 2 (ITS2)"
BASE COUNT      112 a      166 c      164 g      118 t
ORIGIN

Query Match      91.7%; Score 334.8; DB 8; Length 560;
Best Local Similarity 98.4%; Pred. No. 3, 6e-64;
Matches 360; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

OY      1 aaacttcaacaatgagatccttggtccgagcatgaaagaaagcagcgaactgcgat 60
        |||||||
        1 AAACCTTCAACAATGAGATCTTGTTCCGATCGATGAGAAGACGACGCACTGCGAT 60
DB
OY      183 AAACCTTCAACAATGAGATCTTGTTCCGATCGATGAGAAGACGACGCACTGCGAT 242
        |||||||
        183 AAGTAATGTGAATTCACAATTCAGTGAATCATGAGCTTTGAAACGCACATTCGCGCCC 302
DB
OY      61 aagtaatgtaattgcaagaatcagatcatcgaagtccttgaagcacatlgcggccc 120
        |||||||
        61 AAGTAATGTGAATTCACAATTCAGTGAATCATGAGCTTTGAAACGCACATTCGCGCCC 302
DB
OY      121 ctggcatccgaggggagcctgctcgcagagcgtcattgctgcccacaagcccgctgtg 180
        |||||||
        121 CTGGCATTCGGGGGGGAGCTGCTGTCAGAGGCTCATTCCTCCCAAGCCCGGCTTGTG 180
DB
OY      303 ctggcatccgaggggagcctgctcgcagagcgtcattgctgcccacaagcccgctgtg 362
        |||||||
        303 CTGGCATTCGGGGGGGAGCTGCTGTCAGAGGCTCATTCCTCCCAAGCCCGGCTTGTG 362
DB
OY      181 tgttggtcgtcgtcccccgcgggggagcggccgaaagcagcgcgccgctgc 239
        |||||||
        181 TGTTCGCTCCTGCTCCCGCCCGCGGGGACGGGCCAAAGGACGCGCGCACCGCTC 239
DB
OY      363 TGTTCGCTCCTGCTCCCGCCCGCGGGGACGGGCCAAAGGACGCGCGCACCGCTC 419
        |||||||
        363 TGTTCGCTCCTGCTCCCGCCCGCGGGGACGGGCCAAAGGACGCGCGCACCGCTC 419
DB
OY      240 cggctcgcagcgtatggtggttgcacccgctcgaatgaagccggcgccgagcc 299
        |||||||
        240 CGGCTCGCAGCGATGAGGGGCTTGCTGTCACCCGCTGATTAAGCCGCGGCGCCACGCC 479
DB
OY      420 CCGGCTCGCAGCGATGAGGGGCTTGCTGTCACCCGCTGATTAAGCCGCGGCGCCACGCC 479
        |||||||
        420 CCGGCTCGCAGCGATGAGGGGCTTGCTGTCACCCGCTGATTAAGCCGCGGCGCCACGCC 479
DB
OY      300 cggctcgcagcgtatggtggttgcacccgctcgaatgaagccggcgccgagcc 359
        |||||||
        300 CGGCTCGCAGCGATGAGGGGCTTGCTGTCACCCGCTGATTAAGCCGCGGCGCCACGCC 359
DB
OY      480 GGGGCTCCCAACCTTATCTTCTCAGTTGACCTCGATCGATGAGGATACCGCTGAA 539
        |||||||
        480 GGGGCTCCCAACCTTATCTTCTCAGTTGACCTCGATCGATGAGGATACCGCTGAA 539
DB
OY      360 actaa 365
        |||||
        360 ACTTAA 545
DB

RESULT 3
AF138289
LOCUS      AF138289      565 bp      DNA      linear      PLN 11-APR-2000
DEFINITION      Emericella nidulans 18S ribosomal RNA gene, partial sequence;
        internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
        transcribed spacer 2, complete sequence; and 28S ribosomal RNA
        gene, partial sequence.
ACCESSION      AF138289
VERSION      AF138289
KEYWORDS      Aspergillus nidulans.
SOURCE      Aspergillus nidulans.
ORGANISM      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
        Eurotiales; Trichocomaceae; Emericella.
REFERENCE      1 (bases 1 to 565)
AUTHORS      Henry,T., Iwen,P.C. and Hinrichs,S.H.
TITLE      Identification of Aspergillus species using internal transcribed
        spacer regions 1 and 2
JOURNAL      J Clin. Microbiol. 38 (4), 1510-1515 (2000)
MEDLINE      20211684
PUBMED      10747135
REFERENCE      2 (bases 1 to 565)
AUTHORS      Henry,T.J., Iwen,P.C. and Hinrichs,S.H.
TITLE      Direct Submission
JOURNAL      Submitted (26-MAR-1999) Pathology and Microbiology, University of
```


FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç
21, Reus, 43201 - Reus - Tarragona, SPAIN
2 (bases 1 to 558)
AUTHORS Stchigel,A., Cano,J. and Guarro,J.
TITLE A new species of *Emericella* and anomalous strains of *E. quadrilineata*
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..558
/organism="Emericella quadrilineata"
/isolate="soil, Australia"
/strain="IMI 370017"
/db_xref="taxon:41735"
/tissue_type="mycelium/hyphal"
misc_feature 30..181
/note="internal transcribed spacer 1 (ITS1)"
rRNA 182..338
/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
gene 182..338
/gene="5.8S rRNA"
misc_feature 339..558
/note="internal transcribed spacer 2 (ITS2)"
BASE COUNT 112 a 165 c 163 g 118 t
ORIGIN
Query Match 88.4%: Score 322.8: DB 8: Length 558:
Best Local Similarity 98.1%: Pred. No.1.6e-61:
Matches 359: Conservative 0: Mismatches 2: Indels 5: Gaps 3:
OY 1 aaatttcacaatgagatctcttggttcgcgcatcgaatgaagaacgcgaactgcgat 60
DB 182 AAACCTTTCAACATGATCTCTTGTTCCGCATCGATGAAGACGACGAATCGCAT 241
OY 61 aagtaatgtgaattgcgaatcagtgatcagtcagtccttggaacgcacattgcgccc 120
DB 242 AAGTAATGTGAATTCAGAAATTCAGTAATTCAGATCTTTGAACGACCATTTGCCCC 301
OY 121 ctgcacatccgggggagcagctgcgcagcagctcagtcgcctcaagcccgagctgtg 180
DB 302 CTGGCATTTCCGGGGGCGATCGCTGTCGAGCGTATGCTGCGCTCAAGCCGCGTTGTG 361
OY 181 tgttgagtcgctgcctcccccgcgggggagcgagcccgaaagcgagcgagcgacg-gt 239
DB 362 TGTTCGGTCTGTCGT---CCCCCCCCGGGGGACGGCCGCAAGGCGAGCGCGCATCGTCT 418
OY 240 ccggtctcgcagcgtataggggttggtacccgcctcgattagggcgcgcgcgcgcaagc 299
DB 419 CCGGCTCTCGACGTAATGGGGCTTGTTCACCCGCTCGATTAGGGCGCGCGCCGACG 478
OY 300 cggcgctcccaacctatcttcacaggtgacccgcgacgcagtcagtagagatacccgctga 359
DB 479 CGGCGTCTCAACCTTATTTTCTCAGTTGACGTCGAGTCA-GTAGGATACCGGCTGA 537
OY 360 acttaa 365
DB 538 ACTTAA 543
RESULT 6
EN1276063 496 bp DNA linear PLN 09-AUG-2000
LOCUS *Emericella nidulans* 5.8S rRNA gene and ITS 1 and 2, strain M2103.
DEFINITION AJ276063
ACCESSION AJ276063.1 GI:7208819
VERSION 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
KEYWORDS internal transcribed spacer 2; ITS1; ITS2.
SOURCE Aspergillus nidulans.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 496)

AUTHORS Webb,J.S., Nixon,M., Eastwood,I.M., Greenhalgh,M., Robson,G.D. and
Handley,P.S.
TITLE Fungal colonization and biodeterioration of plasticized polyvinyl
chloride
JOURNAL Appl. Environ. Microbiol. 66 (8), 3194-3200 (2000)
MEDLINE 20378616
REFERENCE 2 (bases 1 to 496)
AUTHORS Webb,J.S.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2000) Webb J.S., School of Biological Sciences,
University of Manchester, Stopford Building, Oxford Road,
Manchester M13 0DP, UNITED KINGDOM
FEATURES Location/Qualifiers
source 1..496
/organism="Aspergillus nidulans"
/strain="M2103"
/db_xref="taxon:5072"
/country="United Kingdom"
/tissue_type="Mycelia"
/note="Isolated from plasticised PVC"
misc_feature 1..149
/note="internal transcribed spacer 1, ITS1"
rRNA 150..306
/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
gene 150..306
/gene="5.8S rRNA"
misc_feature 307..496
/note="internal transcribed spacer 2, ITS2"
BASE COUNT 92 a 151 c 150 g 103 t
ORIGIN
Query Match 87.3%: Score 318.8: DB 8: Length 496:
Best Local Similarity 98.3%: Pred. No.1.3e-60:
Matches 344: Conservative 0: Mismatches 2: Indels 4: Gaps 2:
OY 1 aaatttcacaatgagatctcttggttcgcgcatcgaatgaagaacgcgaactgcgat 60
DB 150 AAATTTTCAACAAATGATCTCTTGTTCCGGCATCGATGAAGAACGACGAACTCGAT 209
OY 61 aagtaatgtgaattgcgaatcagtgatcagtcagtccttggaacgcacattgcgccc 120
DB 210 AAGTAATGTGAATTCAGAAATTCAGTAATTCAGATCTTTGAACGACCATTTGCCCC 269
OY 121 ctgcacatccgggggagcagctgcgcagcagctcagtcgcctcaagcccgagctgtg 180
DB 270 CTGGCATTTCCGGGGGCGATCGCTTCCGACGCTCATTTGCTCCCTCAAGCCGCGTTGTG 329
OY 181 tgttgagtcgctgcctcccccgcgggggagcgagcccgaaagcgagcgcgacg-gt 239
DB 330 TGTTCGGTCTGTCGT---CCCCCCCCGGGGGACGGCCGCAAGGCGAGCGCGCACCGTGT 386
OY 240 ccggtctcgcagcgtataggggttggtacccgcctcgattagggcgcgcgcgcgcaagc 299
DB 387 CCGGCTCTCGACGTAATGGGGCTTGTTCACCCGCTCGATTAGGGCGCGCGCGCCGACG 446
OY 300 cggcgctcccaacctatcttcacaggtgacccgcgacgcagtcagtagaagga 349
DB 447 CGGCGTCTCAACCTTATTTTCTCAGTTGACCTCGGATCAGTAGGA 496
RESULT 7
EVJ000932 563 bp DNA linear PLN 12-OCT-1998
LOCUS *Emericella varicolor* 5.8S rRNA gene, ITS1 and ITS2.
DEFINITION AJ000932
ACCESSION AJ000932.1 GI:3757577
VERSION 5.8S rRNA gene; ITS1; ITS2.
KEYWORDS Emericella varicolor.
SOURCE Emericella varicolor.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

REFERENCE	(bases 1 to 563)
AUTHORS	Cano,J.F.
TITLE	Direct Submission
JOURNAL	Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA, FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç 21, Reus, 43201 - Reus - Tarragona, SPAIN
REFERENCE	21. (bases 1 to 563)
AUTHORS	Stehligel,A., Cano,J. and Guarro,J.
TITLE	A new species of <i>Emericella</i> and anomalous strains of <i>E. quadrilineata</i>
JOURNAL	Unpublished
FEATURES	Location/Qualifiers
source	1. .563 /organism="Emericella varilecolor" /strain="IMI 343522" /db_xref="taxon:41726" /rissu_type="mycelium/hyphal" 30. .183 /note="Internal transcribed spacer 1 (ITS1)"
misc_feature	184. .340 /gene="5.8S rRNA" /product="5.8S ribosomal RNA" 184. .340 /gene="5.8S rRNA" 341. .563 /note="Internal transcribed spacer 2 (ITS2)"
gene	
misc_feature	
BASE COUNT	115 a 163 c 163 g 122 t
ORIGIN	
Query Match	86.7%; Score 316.4; DB 8; Length 563;
Best Local Similarity	96.7%; Pred. No. 4.2e-60;
Matches	356; Conservative 0; Mismatches 6; Indels 6; Gaps 3;
1	aaccttcaacatgagctcttggttcgcgcatgataagaacgcagcaactgcgat 60
184	AAACTTTCACACATGAGATCTCTTGCTCCGCATGATGAGACACGACGACATGCCAT 243
61	aagtaatgtaatttcagaaattcagtgaaatcgcagcttcgttaacgcacattgcgccc 120
244	AAGTAATGTCGATTCAGAAATTCAGTGAATCATCGAGCTTTGAACGCACATTCGGCCCC 303
121	ctggcaatccggggggagcatgctgttcgcagagcgctattgtcgtcc- tcaagccggttgt 179
304	CTGGCAATCCGGGGGGGCAATGCTTCGCGAGCTCATTTGCTGCCCTTCAAGCCCGGCTTGT 363
180	gtgttcgagtcgctgcctcccccgcgggggagcggcccgaaagcagcggcgagcacc--g 237
364	GTTTGGTGTGCTGCT---CCCCCGGGGAGAGGGGCCCAAAAGCAGCGCGGCACCGTG 420
238	gttcgagtcctcgcagcgatgaggttggtacccgctcgatlaaggccggcgagcgcca 297
421	TCCGCAATCCCTCAGCGCTAAGGGGGCTTTGTACACCGCTCATTAAGGCGCGCGCGCA 480
298	ggcggagtcctcaaaccttctcttcacaggttcgacctgcgagtcaggtlaagataccgct 357
481	GCCGCGCTCTCCACCTTATTTTCTCAGGTTGACCTCGATCAGTACGATACCGGCT 540
358	gaacttaa 365
541	GAACCTTAA 548
RESULT	8
LOCUS	AF157507 569 bp DNA linear PLN 11-APR-2000
DEFINITION	<i>Aspergillus ustus</i> 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF157507
VERSION	AF157507.1 GI:5163469
KEYWORDS	

SOURCE	Aspergillus ustus.
ORGANISM	Aspergillus ustus.
REFERENCE	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
TITLE	1 (bases 1 to 569)
JOURNAL	Henry,T., Iwen,P.C. and Hinrichs,S.H.
MEDLINE	Identification of Aspergillus species using Internal transcribed
PUBLISHED	spacer regions 1 and 2
REFERENCE	J. Clin. Microbiol. 38 (4), 1510-1515 (2000)
TITLE	20211684
JOURNAL	10747135
FEATURES	2 (bases 1 to 569)
source	Henry,T., Iwen,P.C. and Hinrichs,S.H.
rRNA	Submitted (08-JUN-1999) Pathology and Microbiology, University of
misc_rRNA	Nebraska Medical Center, 986495 Nebraska Medical Center, Omaha, NE
rRNA	68198-6495, Douglas
misc_rRNA	Location/Qualifiers
rRNA	1..569
misc_rRNA	/organism="Aspergillus ustus"
rRNA	/db_xref="taxon:40382"
misc_rRNA	/country="Canada: Alberta"
rRNA	<1..30
misc_rRNA	/product="18S ribosomal RNA"
rRNA	31..186
misc_rRNA	/product="Internal transcribed spacer 1"
rRNA	187..342
misc_rRNA	/product="5.8S ribosomal RNA"
rRNA	343..512
misc_rRNA	/product="Internal transcribed spacer 2"
rRNA	513..>569
misc_rRNA	/product="28S ribosomal RNA"
rRNA	167 c 164 g 125 t
BASE COUNT	113 a
ORIGIN	
Query Match	83.9% Score 306.4; DB: 8; Length 569;
Best Local Similarity	96.7%; Pred. No. 6.9e-58;
Matches 356; Conservative	0; Mismatches 6; Indels 6; Gaps 4;
OY	1 aaacttcacaatgatctccttggttcgcgacatgaagaacagcgaaactgcgat 60
DB	185 AAACTTCAACATGATGTCTTGTTCCGGCATGATGAACAAGCAGCAATCGCAT 244
OY	61 aagtaagtgaattcgagaatcagtagaatacatcgaagtcctttgaacgcacatgcgcc 120
DB	245 AAGTAATGTGAATTGCAGATTCAGATGATCAATCAGACTTTTGAACGCCACATTTGGCCCC 304
OY	121 ctggacatccggaggagcagcctgtcccgagcgatctgtgcc-tcaagccgagctgt 179
DB	305 CTGGCA TTCGGGGGGGAGCATGCTGTCCGAGCGTCATTTGCTGCCCTTCAAAGCCC GGCTTGT 364
OY	180 gtgttggtcgtcgtcccccaccgggggagcagcgccgaaaagcagcggtggcacg-g 238
DB	365 GGTGTGGGTGTCGTCGT---CCCTTCGGGGGAGAGGGGCCAAAAGCAGCGCGCACCGCG 421
OY	239 tcctgacctccggagcgtatgaggctgtgtacccgcgcctagtagggccggcgcgagcag 298
DB	422 TCCGGTCTCTCGAAGCGATATGGGGCTTTGTATACC CGCTCGATTAGAGCGCGCGCGCCGCG 481
OY	299 ccggcgctcccaacttat-ctttctcaggttgtacctcgatcaggttagtaggaataccgct 357
DB	482 CCGCGCTCTCAACCTTTATTATTTACAGAGTTGACCTCGATACAGATAGGATACCGCT 541
OY	358 gaacttaa 365
DB	542 GAACCTTAA 549
RESULT	9
LOCUS	AF261658 549 bp DNA linear PLN 02-MAY-2001
DEFINITION	Aspergillus sp. GI306 small subunit ribosomal RNA gene, partial

QY 240 ccggtcctcagcgtatgaggttgcacccgctcattgagcgccgagcgcacg 299
|||||
Db 398 CCGGCTCTCGACGATGAGCGCTTGTCCACCCGCTCGATTAGGCGCGCGGCGCCACC 457
QY 300 cggcgctccaacctatcttctcaggtt 329
|||||
Db 458 CGGCTCTCGAACCTATTCTTCAGGTT 487

RESULT 11
AF078898
LOCUS AF078898 493 bp DNA linear PLN 11-JUN-2001
DEFINITION Emeritella nidulans environmental isolate C0095 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.85
ribosomal RNA gene and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence.
AF078898
AF078898.1 GI:4092047

ACCESSION
VERSION AF078898.1
KEYWORDS
SOURCE
ORGANISM Aspergillus nidulans.
Aspergillus nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emeritella.
1 (bases 1 to 493)
Zhou, Y., Kong, F., Li, R., Wang, X., Wan, Z. and Wang, D.
Identification of Aspergillus fumigatus and related species by
Nested PCR Targeting Ribosomal DNA Internal Transcribed Spacer
Regions
J. Clin. Microbiol. 39 (6), 2261-2266 (2001)
J. Clin. Microbiol. 39 (6), 2261-2266 (2001)
11376067
2 (bases 1 to 493)
Kong, F., Li, R., Luo, Z. and Wang, D.
Phylogenetic Analysis of Pathogenic Aspergillus
Unpublished
3 (bases 1 to 493)
Luo, Z., Li, R., Kong, F., Li, D., Yoshikazu, H. and Wang, D.
Direct Submission
Submitted (17-JUL-1998) Dermatology, First Hospital of Beijing
Medical University, Xishiku St., Beijing 100034, China

FEATURES
source
1. .493
/organism="Aspergillus nidulans"
/isolate="environmental isolate C0095"
/db_xref="taxon:5072"
<1. .7
/product="18S ribosomal RNA"
8. .160
/note="ITS1"
/product="internal transcribed spacer 1"
161. .317
/product="5.8S ribosomal RNA"
318. .485
/note="ITS2"
/product="internal transcribed spacer 2"
486. .>493
/product="28S ribosomal RNA"
BASE COUNT 93 a 152 c 142 g 106 t
ORIGIN

Query Match 81.0%; Score 295.6; DB 8; Length 493;
Best Local Similarity 97.6%; Pred. No. 1.7e-55;
Matches 322; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

QY 1 aaacttcaacaatgagatctctgtgtccgcatcgaagaagcagcgaactgcat 60
|||||
Db 161 AAACCTTCAACATGATGATCTCTGTTCCGCAATCGATGAAGCAACGAACTCGAT 220
QY 61 aagtaatgtaattgcgaattcaagtgaatcagcagctcttgaagcagcattgcgccc 120
|||||
Db 221 AAGTAATGTAATTCAGATTCAGTAATCATCGAGTCTTTGAACGACGCAATTGCGCCC 280

QY 121 ctggcattccgggggycatgctgtccgagagctcatgtctgcctcaagccggctgtg 180
|||||
Db 281 CTGGCAATTCGGGGGGGCAATGCTCTCGAAGCTCATTTGCTGCCCTCAACCCGGCTTGTG 340
QY 181 tcttggtctgtctcccccgcgggggacgggcccgaagaagcagcggcggcggc 239
|||||
Db 341 TCTTGGGTGCTGCT---CCGCCCGGGGGGACGGGCCGAAGGCAACGGCGCACCGTGT 397
QY 240 ccggtcctcagcgtatgaggttgcacccgctcattgagcgccgagcgcacg 299
|||||
Db 398 CCGGCTCTCGACGATGAGCGCTTGTTCACCCGCTCGATTAGGCGCGCGGCGCCACC 457
QY 300 cggcgctccaacctatcttctcaggtt 329
|||||
Db 458 CGGCTCTCGAACCTATTCTTCAGGTT 487

RESULT 12
AF033428
LOCUS AF033428 1148 bp DNA linear PLN 13-FEB-2001
DEFINITION Penicillium implicatum strain NRRL 2061 internal transcribed spacer
1, 5.8S ribosomal RNA gene and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence.
AF033428
AF033428.1 GI:2668668

ACCESSION
VERSION AF033428
KEYWORDS
SOURCE
ORGANISM Penicillium implicatum.
Penicillium implicatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
1 (bases 1 to 1148)
Peterson, S.W.
Phylogenetic analysis of Penicillium species based on ITS and
LSU-rDNA nucleotide sequences
(in) Samson, R.A. and Pitt, J.I. (Eds.):
INTEGRATION OF MODERN TAXONOMIC METHODS FOR PENICILLIUM AND
ASPERGILLUS CLASSIFICATION: 163-178;
Harwood Academic Publishers, The Netherlands (2000)

REFERENCE
AUTHORS Peterson, S.W.
TITLE 1su-rDNA nucleotide sequences
JOURNAL Unpublished
3 (bases 1 to 1148)
Peterson, S.W.
Direct Submission
Submitted (07-NOV-1997) Microbial Properties Research, National
Center for Agricultural Utilization Research, 1815 N. University
St., Peoria, IL 61604, USA

FEATURES
source
1. .1148
/organism="Penicillium implicatum"
/strain="NRRL 2061"
/db_xref="taxon:69775"
1. .187
/product="internal transcribed spacer 1"
188. .344
/product="5.8S"
345. .514
/product="internal transcribed spacer 2"
515. .>1148
/product="28S"
BASE COUNT 237 a 338 c 360 g 213 t
ORIGIN

Query Match 79.7%; Score 290.8; DB 8; Length 1148;
Best Local Similarity 92.4%; Pred. No. 1.8e-54;
Matches 340; Conservative 0; Mismatches 22; Indels 6; Gaps 3;

QY 1 aaacttcaacaatgagatctctgtgtccgcatcgaagaagcagcgaactgcat 60
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Db 188 AAACCTTCAACATGATGATCTCTGTTCCGCAATCGATGAAGCAACGCAAAATGCGAT 247

[illegible]

```

RESULT 13
LOCUS      AEU65310                      581 bp      DNA      linear      PLN 01-JAN-1998
DEFINITION Aspergillus ellipticus Internal transcribed spacer 1, partial
            sequence, 5.8S ribosomal RNA gene and internal transcribed spacer
            2, complete sequences, and 25S ribosomal RNA gene, partial
            sequence.
ACCESSION  U65310
VERSION     U65310.1
KEYWORDS    GI:2737898
SOURCE      '
            Aspergillus ellipticus.
            Aspergillus ellipticus
            Aspergillus ellipticus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
            1 (bases 1 to 581)
            Peterson,S.W.
            Aspergillus subgenus Circumdati section Nigri: relationships based
            upon nuclear DNA complementarity and rDNA sequence analysis
            unpublished
            2 (bases 1 to 581)
            Peterson,S.W.
            Direct Submission
            Submitted (26-JUL-1996) Microbial Properties, NCAR, 1815 N.
            University St., Peoria, IL 61604, USA
FEATURES
    source
        1..581
            /organism="Aspergillus ellipticus"
            /strain="NRRL 5120"
            /db_xref="taxon:41066"
            <1..197
            /note="Internal transcribed spacer 1; ITS1"
            198..354
            /product="5.8S ribosomal RNA"
            355..531
            /note="Internal transcribed spacer 2; ITS2"
            532..>581
            /product="25S ribosomal RNA"
BASE COUNT 112 a      179 c      166 g      124 t
ORIGIN
Query Match      78.9%; Score 288; DB 8; Length 581;
Best Local Similarity 92.1%; Pred. NO. 8e-54; 25; Indels 4; Gaps 3.
Matches 337; Conservative
1 aaacttcaacatgatctctgtgttcgcgatcatgaagaacgcagactgcat 60

```

Db	198	AAACTTTCACAAATGAGATCTCTTGGTTCGGCATTCGATGAAGAAACGACGGAATGCGAT	257
Qy	61	aaglaatgtaattgatacgaatcagtgaaatcatcagatcgaagtccttgaaagcacatctgagccc	120
Db	258	AACATATGTGAATTGCAGAAATTCAAGTGAATCATGTAGACTCTTTGAAACGACCATTTGCGCCC	317
Qy	121	cttgacatccgggggggacatgcctctgtccgaagcgtcaattgcttgccctcaagccgggcttggtg	180
Db	318	CTGCAATTCGCGGGGGGCAATGCTCTCCGAGCGTCAATTGCTGCCCTCAAGCGCCGGCTTGTG	377
Qy	181	ttgttggtgcgtcgtcccccccccccggggggaagcgccgaaaggaagcgagcgaccg-qt	239
Db	378	TGTTGGGTGCGCGTCCCATCCCGGGGAGCGGCCCGAAGAGCAGCGGCGCACCCGCT	437
Qy	240	ccggcctcccgagcgtatgggcttgtaaccgcctcgatlaaggccggccgagcgccagc	299
Db	438	CCGATCCTCGAGCGATGGGGCTTTGTACCCGCTC--TGTAGSACCGCGCGGGCGCTGC	495
Qy	300	cggcgctcccaacctatccttctcaagltgacatcggaatcaagtlaagabacccgctga	359
Db	496	CGACGTTTTCACAC-CATTTTTCAGAGTGACCTCGGATCAGGTAGGATATACCCGCTGA	554
Qy	360	actaa 365	
Db	555	ACTTAA 560	

RESULT	14	
AF033421		1110 bp DNA linear PLN 13-FEB-2001
LOCUS		
DEFINITION		Penicillium sartoryi strain NRRL 783 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION		AF033421
VERSION		AF033421.1 GI:2668661
KEYWORDS		
SOURCE		.
ORGANISM		Penicillium sartoryi.
		Penicillium sartoryi
		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
		Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium
REFERENCE		1 (bases 1 to 1110)
AUTHORS		Peterson,S.W.
TITLE		Phylogenetic analysis of Penicillium species based on ITS and LSU-rDNA nucleotide sequences
JOURNAL		(in) Samson,R.A. and Pitt,J.I. (Eds.):
		INTEGRATION OF MODERN TAXONOMIC METHODS FOR PENICILLIUM AND ASPERGILLUS CLASSIFICATION: 163-178;
		Harwood Academic Publishers, The Netherlands (2000)
REFERENCE		2 (bases 1 to 1110)
AUTHORS		Peterson,S.W.
TITLE		Phylogenetic analysis of Penicillium species based on ITS and LSU-rDNA nucleotide sequences
JOURNAL		Unpublished
REFERENCE		3 (bases 1 to 1110)
AUTHORS		Peterson,S.W.
TITLE		Direct Submission
JOURNAL		Submitted (07-NOV-1997) Microbial Properties Research, National Center for Agricultural Utilization Research, 1815 N. University St., Peoria, IL 61604, USA
FEATURES		Location/Qualifiers
Source		1..1110
		/organism="Penicillium sartoryi"
		/strain="NRRL 783"
		/db_xref="taxon:70101"
		1..150
misc_RNA		/product="internal transcribed spacer 1"
		151..307
rRNA		/product="5.8S"
		308..476
misc_RNA		/product="internal transcribed spacer 2"
		477..>1110
rRNA		/product="28S"
BASE COUNT		240 a 314 c 218 t

ORIGIN

Query Match	78.68;	Score 286.8;	DB 8;	Length 1110;
Best Local Similarity	91.88;	Pred. No. 1.4e-53;		
Matches 336;	Conservative	0;	Mismatches 27;	Indels 3;
				Gaps 3;

Oy	1	aaacttccaacatgatctcttggctccgagatcgaagaaacgacgaactcgat	60
Db	151	AAACTTTCAACAACGGATCTTGGTCCGGATGATGAAGAAGCAAGCAATATGGAT	210
Oy	61	aagbaabgtyaatctgcagaatcagtgaaatcagagtccttgaacgacacattgcgccc	120
Db	211	AACTAATGTAATTGCAGAAATTCAGTGAATCATCCAGCTTTGAACCCACATATGGCGCTT	270
Oy	121	ctggacatccggggggcattgctctgcgagcgtaattgtctgcctcaagccggattgtg	180
Db	271	CTGGTAATTCGGAGGGGCATGCTGTCCAGGCTCATTTCTCCCTCAAGCCCGGCTTGTG	330
Oy	181	tgtttggatcg tgc tcccccceccggggggaacggagccgaagaagcagcgcgacacg -gt	239
Db	331	TGTTGGGGCCCCGTCGCCCCGCCGGGGGAGCAGCGCCCAAAAGCAGCGCGCAGCACCGCT	390
Oy	240	ccggatccctcagcgctatgggagcttggctcaaccgcgcctcgaattagggccggccggcgccagc	299
Db	391	CCGGTCTTCAGCGGTATGGGGCTTGCTACACCGGCTCTAGTAGGCCCGGACC -GGCGCCAGC	449
Oy	300	cgagcgctcccaacctatcttctcaagttgaactcggatcaggtatggataaccgcgtga	359
Db	450	CGAC -CCCCAACCTTAATTATCTCAGTTGACCTCGGATAGGATAGGAGATACCCGCTGA	508
Oy	360	acttaa	365
Db	509	ACTTAA	514

RESULT	15
AF033422	1110 bp DNA linear PLN 13-FEB-2001
LOCUS	
DEFINITION	Penicillium citrinum strain NRRL 1841 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF033422
VERSION	AF033422.1 GI:2668662

misc_RNA	1.150	/product="internal transcribed spacer 1"
rRNA	151.307	/product="5.8S"
misc_RNA	308.476	/product="internal transcribed spacer 2"
rRNA	477.2110	/product="28S"
BASE COUNT	241 a 313 c 338 g 218 t	
ORIGIN		

Query Match	78.68;	Score 286.8;	DB 8;	Length 1110;
Best Local Similarity	91.88;	Pred. No. 1.4e-53;		
Matches 336;	Conservative 0;	Mismatches 27;	Indels 3;	Gaps 3;

QY	1	aaacttccaacaatggatctctctggttcgcgcgacatctgaagaacgcagagaaatgcgat	60
Db	151	AAACTTTCACACAGCGATCTCTTGTTGCCGCATCGATGAAAGAACGACGGAATGCGAT	210
QY	61	aaglaatgtgaattgtcgaatctcagtgaaatcatcgaagtccttctgaacgcacattgcgcc	120
Db	211	AACTAATGTGAATTGCGAAGATTCTAGTGAATCATCATGAGTCTTTGAAACGACATTTGCCCTT	270
QY	121	ctgagcatctcgggggggcattgcctgtccgaagcgttcattgtcgtgccttaagccgggtttgtg	180
Db	271	CTGGTAATCCCGAGGCGCATGCTCTCCGAGCGTCAATTGCTGCCCTCAAGCCCGGCTTTGTG	330
QY	181	tgtttaggtcgtcgtctccccccccccggggggaacgggcccgaagacagagggcggacacg	239
Db	331	TGTTGGGCCCCCTCCCCCCCGGGGGGACGGGCCGGAAGGCAAGCGCGGCACCCGCT	390
QY	240	ccggctcctcagacglatagggctgtgtcaaccgcctcgaatlagggcggccggcgccagc	299
Db	391	CCGGTCCTCGAGCGATGGGGCTTCGTACCCCGCTCAATGAGGCCCGGCC	449
QY	300	cggcgctctcaaccttattcttcgaagtttgacctcggatcaggttaaggataaccgcgtga	359
Db	450	CGAC-CCCAACCTTTATATTCTCAGATGCACTCGGATCAGGTAGGATACCCGCTGA	508
QY	360	acttaa	365
Db	509	ACTTAA	514

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 20:46:20 ; Search time 594.49 Seconds
(without alignments)
1054.137 Million cell updates/sec

Title: US-10-046-955-5

Perfect score: 365
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Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapept 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_032802.*
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4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365	100.0	365	20	AAV70849
2	284.2	77.9	365	20	AAV70847
3	258.8	70.9	364	20	AAV70846
4	256	70.1	355	20	AAZ22438
5	230.4	63.1	355	20	AAV70848
6	221.2	60.6	382	21	AAV72782
7	220.6	60.4	498	20	AAZ22437
8	206.8	56.7	610	20	AAV90111
9	206.6	56.6	309	20	AAV70872

10	203.8	55.8	568	20	AAV90112
11	195.2	53.5	640	22	AAH73767
12	188.4	51.6	608	20	AAV90110
13	184	50.4	618	22	AAH73768
14	180.6	49.5	597	19	AAV43265
15	180.2	49.4	561	19	AAV59009
16	179.4	49.2	553	21	AAZ91726
17	179.2	49.1	582	18	AAV65100
18	177.8	48.7	549	21	AAZ91723
19	177.8	48.7	549	21	AAZ91724
20	176	48.2	537	21	AAZ91725
21	174.4	47.8	590	20	AAZ11797
22	171.8	47.1	615	22	AAV76260
23	171	46.8	2293	23	AAZ16211
24	170.4	46.7	579	20	AAZ11794
25	170	46.6	569	18	AAV65101
26	169.6	46.5	580	20	AAZ11793
27	169.4	46.4	578	24	ABA01155
28	169.2	46.4	579	20	AAZ11785
29	169.2	46.4	579	20	AAZ11786
30	169.2	46.4	579	20	AAZ11790
31	169.2	46.4	579	20	AAZ11792
32	169.2	46.4	579	22	AAV08425
33	168.8	46.2	579	20	AAZ11788
34	168	46.0	580	20	AAZ11796
35	167.6	45.9	545	16	AAV05403
36	167.2	45.8	579	20	AAZ11787
37	166.8	45.7	588	19	AAV43267
38	166.6	45.6	580	20	AAZ11789
39	166.4	45.6	588	19	AAV43266
40	166.4	45.4	548	16	AAV05394
41	165.8	45.4	548	19	AAV62501
42	165.8	45.4	548	22	AAV08424
43	165.6	45.4	556	12	AAV59008
44	165.6	45.4	556	19	AAV62594
45	165.4	45.3	626	16	AAV05396

ALIGNMENTS

RESULT 1	AAV70849
ID	AAV70849 standard; DNA; 365 BP.
XX	
AC	AAV70849;
XX	
DT	26-FEB-1999 (first entry)
XX	
DE	Sequence containing the rDNA internal transcribed spacer 2 (ITS2).
XX	
KW	5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
KW	28S ribosomal RNA gene; probe: Aspergillus flavus; A. fumigatus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;
KW	M. circinellioides f. circinellioides; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Aspergillus nidulans.
XX	
PN	WO9805084-A2.
XX	
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	
PR	02-MAY-1997; 97US-0045400.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Aldorevich L, Choi JS, Morrison CJ, Relas E;

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XX
DR   WPI; 1999-034737/03.
XX
XX   New nucleic acid probes for filamentous fungi - for detecting e.g.
PT   Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT   Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT   species.
XX
XX   Claim 1; Page 11; 45pp; English.
XX
XX   The present sequence represents a partial 5.8S ribosomal RNA gene,
CC   internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
CC   gene. Probes can be derived from the present sequence which are
CC   species-specific. The specification also describes ITS2 sequence-derived
CC   probes for identifying a species selected from Aspergillus flavus,
CC   A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani,
CC   F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus,
CC   M. circinalis, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera,
CC   Cunninghamella elegans, Pseudallescheria boydii (teleomorph of
CC   Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenckii.
CC   The probes can be used for differentiating filamentous fungal species
CC   from each other and from other medically important fungi.
XX
XX   Sequence 365 BP; 68 A; 109 C; 109 G; 79 T; 0 other:
SQ
Query Match          100.0%; Score 365; DB 20; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY   1 aaacttcaacaatgatactcttgggttcgagcatgatgaagaacgacgcaactgcgat 60
DB   1 aaacttcaacaatgatactcttgggttcgagcatgatgaagaacgacgcaactgcgat 60
OY   61 aagtaatgtaattgcaatgcaatcagatcatcagatctttaaagcagatgcgcccc 120
DB   61 aagtaatgtaattgcaatgcaatcagatcatcagatctttaaagcagatgcgcccc 120
OY   121 ctggcattccgggggagcagtcgctgcgagcgatcgtctgcctccaagccggcttg 180
DB   121 ctggcattccgggggagcagtcgctgcgagcgatcgtctgcctccaagccggcttg 180
OY   181 tgttggtcgtcgtcccccgggggagcgagccgaaagcagcgcgacgcgtc 240
DB   181 tgttggtcgtcgtcccccgggggagcgagccgaaagcagcgcgacgcgtc 240
OY   241 cggctcccgagcgatgagggcttgatcagcgtcgatgaaggccggcgagccagcc 300
DB   241 cggctcccgagcgatgagggcttgatcagcgtcgatgaaggccggcgagccagcc 300
OY   301 ggcgtctcaaaccttattcttcaaggttgacctcgatcaggtaggaataccgcgtgaa 360
DB   301 ggcgtctcaaaccttattcttcaaggttgacctcgatcaggtaggaataccgcgtgaa 360
OY   361 cttaa 365
DB   361 cttaa 365

RESULT 2
AAV70847
ID   AAV70847 standard; DNA; 365 BP.
XX
AC   AAV70847;
XX
DT   26-FEB-1999 (first entry)
XX
DE   Sequence containing the rDNA internal transcribed spacer 2 (ITS2).
XX
XX   5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
KM   28S ribosomal RNA gene; probe; Aspergillus flavus; A. fumigatus;
KM   A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;

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KM   Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;
KM   M. circinalis; M. circinaloides; Rhizopus oryzae; R. microsporus;
KM   R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KM   Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KM   Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
XX   Aspergillus niger.
XX
XX   WO9850584-A2.
XX
XX   12-NOV-1998.
XX
XX   01-MAY-1998; 98WO-US08926.
XX
XX   02-MAY-1997; 97US-0045400.
XX
XX   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX   Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX
XX   WPI; 1999-034737/03.
XX
XX   New nucleic acid probes for filamentous fungi - for detecting e.g.
PT   Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT   Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT   species.
XX
XX   Claim 1; Page 10-11; 45pp; English.
XX
XX   The present sequence represents a partial 5.8S ribosomal RNA gene,
CC   internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
CC   gene. Probes can be derived from the present sequence which are
CC   species-specific. The specification also describes ITS2 sequence-derived
CC   probes for identifying a species selected from Aspergillus flavus,
CC   A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani,
CC   F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus,
CC   M. circinalis, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera,
CC   Cunninghamella elegans, Pseudallescheria boydii (teleomorph of
CC   Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenckii.
CC   The probes can be used for differentiating filamentous fungal species
CC   from each other and from other medically important fungi.
XX
XX   Sequence 365 BP; 71 A; 106 C; 103 G; 85 T; 0 other:
SQ
Query Match          77.9%; Score 284.2; DB 20; Length 365;
Best Local Similarity 91.3%; Pred. NO. 1.8e-75;
Matches 335; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

OY   1 aaacttcaacaatgatactcttgggttcgagcatgatgaagaacgacgcaactgcgat 60
DB   1 aaacttcaacaatgatactcttgggttcgagcatgatgaagaacgacgcaactgcgat 60
OY   61 aagtaatgtaattgcaatgcaatcagatcatcagatctttaaagcagatgcgcccc 120
DB   61 aagtaatgtaattgcaatgcaatcagatcatcagatctttaaagcagatgcgcccc 120
OY   121 ctggcattccgggggagcagtcgctgcgagcgatcgtctgcctccaagccggcttg 180
DB   121 ctggcattccgggggagcagtcgctgcgagcgatcgtctgcctccaagccggcttg 180
OY   181 tgttggtcgtcgtcccccgggggagcgagccgaaagcagcgcgacgcgtc 240
DB   181 tgttggtcgtcgtcccccgggggagcgagccgaaagcagcgcgacgcgtc 240
OY   241 cggctcccgagcgatgagggcttgatcagcgtcgatgaaggccggcgagccagcc 298
DB   241 cggctcccgagcgatgagggcttgatcagcgtcgatgaaggccggcgagccagcc 298
OY   299 cggagctccaaccttattcttcaaggttgacctcgatcaggtaggaataccgcgtg 358
DB   299 cggagctccaaccttattcttcaaggttgacctcgatcaggtaggaataccgcgtg 358

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Oy 359 aacttaa 365
Db 359 aacttaa 365

RESULT 3

AAV70846
ID AAV70846 standard; DNA; 364 BP.

AAV70846;

26-FEB-1999 (first entry)

Sequence containing the rDNA Internal transcribed spacer 2 (ITS2).

5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
28S ribosomal RNA gene; probe; *Aspergillus flavus*; *A. fumigatus*;
A. niger; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*;
Mucor rouxii; *M. racemosus*; *M. plumbeus*; *M. indicus*;
M. circinelloides f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;
R. circinans; *R. stolonifer*; *Rhizomucor pusillus*; *Ascidia corymbifera*;
Cunninghamella elegans; *Pseudallescheria boydii*; *Scedosporium apiospermum*;
Penicillium notatum; *Sporothrix schenckii*; filamentous fungus; ss.

Aspergillus fumigatus.

WO9850584-A2.

12-NOV-1998.

01-MAY-1998: 98WO-US08926.

02-MAY-1997: 97US-0045400.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Aldorevich L, Choi JS, Morrison CJ, Reiss E;

WPI: 1999-034737/03.

New nucleic acid probes for filamentous fungi - for detecting e.g.

Aspergillus, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Ascidia*,

Cunninghamella, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*

species.

Claim 1: Page 10: 45pp: English.

The present sequence represents a partial 5.8S ribosomal RNA gene,
internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
gene. Probes can be derived from the present sequence which are
species-specific. The specification also describes ITS2 sequence-derived
probes for identifying a species selected from *Aspergillus flavus*,
A. fumigatus, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*,
F. moniliforme, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*,
M. circinelloides f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*,
R. circinans, *R. stolonifer*, *Rhizomucor pusillus*, *Ascidia corymbifera*,
Cunninghamella elegans, *Pseudallescheria boydii* (teleomorph of
Scedosporium apiospermum), *Penicillium notatum*, or *Sporothrix schenckii*.
The probes can be used for differentiating filamentous fungal species
from each other and from other medically important fungi.

Sequence 364 BP: 74 A; 107 C; 102 G; 81 T; 0 other;

Query Match 70.9%; Score 258.8; DB 20; Length 364;
Best Local Similarity 90.5%; Pred. No. 7.3e-68;
Matches 333; Conservative 0; Mismatches 27; Indels 8; Gaps 5;

Oy 1 aaacttcaacatgatctcttggttcgcgcatcgaagaagcagcggaactgcgat 60
Db 1 aaacttcaacatgatctcttggttcgcgcatcgaagaagcagcggaactgcgat 60

Oy 61 aagtaatgtgaattgcagaattcagatgaatcatcgaatctcttgaaacgacattgcgcc 120
Db 61 aactaatgtgaattgcagaattcagatgaatcatcgaatctcttgaaacgacattgcgcc 120
Oy 121 ctggcattccggggggaactgctctccgaagcattatgctgcgcc--tcaagccggcctgt 179
Db 121 ctggtatctccggggggaactgctctccgaagcattatgctgcgcc--tcaagccggcctgt 180
Oy 180 gtgttggttcgtctccccc--cccccgggggaagcagcggaagcagcgcgacacg- 237
Db 181 gtgttggttcgtctccccc--cccccgggggaagcagcggaagcagcgcgacacg- 240
Oy 238 gtccggtctcgaagcgtatgggctgtgtaaccgcctgattaggcgcggcgagcgca 297
Db 241 gtccggtctcgaagcgtatgggctgtgtaaccgcctgattaggcgcggcgagcgca 297
Oy 298 gccgagcgtccaaacctatcttctcgaagttgaccccgatcaggaaggaataccgct 357
Db 298 gccgac--accgaactatcttctcgaagttgaccccgatcaggaaggaataccgct 355
Oy 358 gaacttaa 365
Db 356 gaacttaa 363

RESULT 4

AA222438
ID AA222438 standard; DNA; 556 BP.

AA222438;

02-DEC-1999 (first entry)

Internal Transcribed Spacer of *P. expansum*.

Internal Transcribed Spacer: ITS; fungus; yeast; fermentation; assay;

PCR; microorganism; wine-making; commercial; ds.

Penicillium expansum.

WO9946405-A1.

16-SEP-1999.

11-MAR-1999: 99WO-US04251.

11-MAR-1998: 98US-0037990.

(GALL-) GALLO WINERY E & J.

Engel SR, Descenzo RA, Morenzoni RA, Ireland NA;

WPI: 1999-551425/46.

New isolated fungal and yeast nucleic acids, used for identifying

different fermentation-related microorganisms, particularly in wine

fermentation cultures -

Disclosure; Page 32-33; 52pp: English.

This is the nucleotide sequence for the Internal Transcribed Spacer
(ITS) of *P. expansum*. This sequence was amplified directly from the
isolate by the ITS5 (AA222530) and ITS4 (22531) primers.
This invention is directed to the identification of different
fermentation-related microorganisms, particularly those involved in the
production of wine. The invention utilizes a polymerase chain reaction
(PCR) based diagnostic assay of DNA sequences located in the Internal
Transcribed Spacer (ITS) region of the ribosomal RNA gene.
Ribosomal genes are suitable for use as molecular probe targets because
of their high copy number. Non transcribed and transcribed spacer
sequences associated with ribosomal genes are usually poorly conserved
and, thus, are advantageously used as target sequences for the detection
of recent evolutionary divergence. Fungal RNA genes are organized in

CC units. Each unit encodes mature subunits of 18S, 5.8S and 28S rRNA. The
CC
17S region lies between the 18S and 28S rRNA genes and contains two
CC variable non-coding spacers (ITS1 and ITS2) and the 5.8S rRNA gene.
XX
Sequence 556 BP; 111 A; 168 C; 155 G; 122 T; 0 other;

Query Match	70.18;	Score 256;	DB 20;	Length 556;
Best Local Similarity	88.58;	Pred. No. 5.8e-67;		
Matches 324;	Conservative	0;	Mismatches 35;	Indels 7;
				Gaps 4

QY	1	aaacttcaacaatggtcctcttggtcttcgggcacatcgaatgaagaacggaactgcat	60
Db	175	aaacttcaacaacgagatcctcttggtcttcgggcacatcgaatcgaacggaacgaatgcat	234
QY	61	aagtaatgtagaattgcagaaattcagttgaatcatcgaatcctttgaacgcacatgagcccc	120
Db	235	acgttaatgtagaattgcacaaattcagttgaatcatcgaatcctttgaacgcacatgagcccc	293
QY	121	ctggcatctcgggggggacatgcctgctccgaagctcatctgctgcctctcaagcccgctgtg	180
Db	294	ctggatattccggggggacatgcctgtccgaagctcatctgctgcctctcaagcccgctgtg	353
QY	181	tgtttgggtgcgtgcgtcccccgcgggggagcgggcccgaagaagcagcgcgacacgg-gt	239
Db	354	tgtttgggtgcgtgcgtcccccgcgggggagcgggcccgaagaagcagcgcgacacgg-gt	413
QY	240	cgggttccctcagagcggtatggggcgctgtgtccacccgctctgaatlaggcggcgccgggcgcagc	299
Db	414	cgggttccctcagagcggtatggggcgctgtgtccacccgctctgaatlaggcggcgccgggcgcctgc	471
QY	300	cggggtctcccaacattactttctcaggtcttgacctcggatccaggtaaagataaccgctga	359
Db	472	cggatcaaccaccaattcttattccaggtcttgacctcggatccaggtaaagataaccgctga	528
QY	360	actctaa	365
Db	529	actctaa	534

XX	RESULT	5	
XX	AAV70848		
ID	AAV70848	standard;	DNA: 355 BP.
XX			
XX	AAV70848;		
XX			
DT	26-FEB-1999	(first entry)	
XX			
DE	Sequence containing the rDNA internal transcribed spacer 2 (ITS2).		
XX			
KW	5.8S ribosomal RNA gene; Internal transcribed spacer 2; ITS2;		
KW	28S ribosomal RNA gene; probe: Aspergillus flavus; A. fumigatus;		
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;		
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;		
KW	M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;		
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;		
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;		
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.		
XX			
OS	Aspergillus terreus.		
XX			
PN	MO9850584-A2.		
XX			
PD	12-NOV-1998.		
XX			
PF	01-MAY-1998; 98MO-US08926.		
XX			
PR	02-MAY-1997; 97US-0045400.		
XX			
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX			
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;		

DR WPI; 1999-034737/03.
XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Absidia*,
PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*
PT species.

Claim 1; Page 11; 45pp; English.

CC The present sequence represents a partial 5.8S ribosomal RNA gene,
CC internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
CC gene. Probes can be derived from the present sequence which are
CC species-specific. The specification also describes ITS2 sequence-derived
CC probes for identifying a species selected from *Aspergillus flavus*,
CC *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*,
CC *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*,
CC *M. circinaloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*,
CC *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Aspidia corymbifera*,
CC *Cunninghamella elegans*, *Pseudallesheria boydii* (telomorph of
CC *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*.
CC The probes can be used for differentiating filamentous fungal species
CC from each other and from other medically important fungi.

50 Sequence 355 BP; 62 A; 105 C; 103 G; 85 T; 0 other;

Query Match	63.18;	Score 230.4;	DB 20;	Length 355;
Best Local Similarity	87.68;	Pred. No. 2.3e-59;		
Matches 312; Conservative	0;	Mismatches 31;	Indels 13;	Gaps 5

QY 1 aaacttcaacaatgacatctcttctgttcgcgcacatcgatagaagaacgcagcgaactcgcat 60

DG 1 aaactttccaacaatgaca-ctctctgtcttcgcgcacatcgatagaagaacgcagcgaatctcgat 60

QY 61 aagtaatgtgaaattcgacgaatttcgaatcgaatcgaatcgaatctcttgaagccacattcgcccc 120

DG 61 aactaatgtgaatttcgcgaatttcgcgaatttcgaatcgaatcgaatcgaatctcttgaagccacattcgcccc 120

QY 121 ctgcgcatctccggg-gggagatgcctgcgtccgcagcgatcatctctgcctccaagcccggtctgt 175

DG 121 ctggtatctccgggggggcagtgcgtccgcagcgatcatctctgcctccaagcccggtctgt 180

QY 180 gttcttggtgcctgcctgcctccc--cccaccggggagacggcccgaaagcagcggcggcaccg 237

DG 181 gttcttggtgcctgcctgcctcccgcgtcccccggggagacggcccgaaagcagcggcggcaccg 240

QY 238 -gtccgggtccctggaacgcatatggggcttgggtcacccgcgtcgatlaaggccgcgggcggcc 290

DG 241 cgtcccggtccctcgagaagcgtatggggcttgcgtcttcgcgtc-cgtlaaggccgcgggcggcc 295

QY 297 agccggcgcgtctca-----aacctaatctctcaaggtttagaccctggacgaaggt 344

DG 300 gccggaacgattatcttcgaactcgtttcttcttccaaggtttgaccctggacgaaggt 355

RESULT	6
AAA72782	
ID	AAA72782 standard; DNA; 382 BP.

AC	AAA72782;
XX	
DT	13-DEC-2000 (first entry)
XX	
DE	5.8s rRNA gene sequence.
XX	
KM	Black spot disease; brown spot disease; fungi; fruit vegetable;
XX	
KM	field crop; Alternaria; 5.8s rRNA; detection; ds.
XX	
OS	Aspergillus flavus.
XX	
PN	MO200046397-A1.
XX	
PD	10-AUG-2000.

```
XX 24-JAN-2000: 2000HO-US01466.
PF XX
XX 02-FEB-1999: 990US-0241427.
PR XX
XX (TECR ) TECHNION RES & DEV FOUND LTD.
PA (KASH/) KASHI Y.
XX XX
PI Kashi Y, Zur G, Sharf R, Hallerman E;
XX XX
DR WPI: 2000-499381/44.
XX XX
PT Nucleic acid based assay and kit for detection of Alternaria
PT contamination in food products involves analysing the sample of food
PT product for nucleic acid sequences unique to Alternaria
XX XX
XX Examples: Fig 1: 47pp; English.
XX XX
CC The invention relates to a nucleic acid based method for the detection
CC of Alternaria contamination in a food product. The method involves
CC obtaining and analysing a food product sample for a nucleic acid sequence
CC unique to Alternaria. Detectable levels of the nucleic acid sequence can
CC be used as an indication of Alternaria contamination. Fungi from the
CC genus Alternaria are ubiquitous saprophytes and are economically
CC important pathogens affecting a wide range of plants. Alternaria are the
CC causative agents of black or brown spot disease in many fruits,
CC vegetables and field crops. The method is used for the detection of
CC Alternaria contamination in food products. The present sequence
CC represents the Aspergillus flavus 5.8S rRNA gene, used in examples
CC illustrating the invention.
XX XX
SO Sequence 382 BP: 72 A; 111 C; 114 G; 84 T; 1 other:

Query Match 60.6%; Score 221.2; DB 21: Length 382;
Best Local Similarity 94.2%; Pred. No. 1.4e-56;
Matches 262; Conservative 0; Mismatches 13; Indels 3; Gaps 3;

QY 1 aaacttcaacaatgagatcctctgttcgcgcatcgatgaagaacgacgacatgcgat 60
DB 98 aaacttcaacaatgagatcctctgttcgcgcatcgatgaagaacgacgacatgcgat 157
QY 61 aagtaatgtgaattgagaatcagatcagatcagatcgtttgaaagcagatgcgcc 120
DB 158 aactatgtgaattgagaatcagatcagatcagatcgtttgaaagcagatgcgcc 217
QY 121 ctggatctcgggggagcagatcgttcgagcgatcgttcgtcc-ccaagcccgctgtg 179
DB 218 ctggatctcgggggagcagatcgttcgagcgatcgttcgtccccaagcagcgctgtg 277
QY 180 gtgttggtcgtcgtccccc-cgccccggggagcagcgccgaaagcagcgcgacagc- 237
DB 278 gtgttggtcgtcgtcccccctcccgggggagcagcgccccaagcagcgcgacagc 337
QY 238 gtccggtcctcgagcgatcgagggctgttcacccgctc 275
DB 338 gtccggtcctcgagcgatcgagggctgttcacccgctc 375

RESULT 7
AA222437
ID AA222437 standard; DNA: 498 BP.
AC AA222437;
XX XX
DT 02-DEC-1999 (first entry)
XX XX
DE Internal Transcribed Spacer of P. crustosum.
XX XX
KW Internal Transcribed Spacer; ITS: fungus; yeast; fermentation; assay;
XX PCR; microorganism; wine-making; commercial; ds.
OS Penicillium crustosum.
```

```
XX XX
XX WO9946405-A1.
XX XX
XX 16-SEP-1999.
XX XX
XX 11-MAR-1999; 99WO-US04251.
XX XX
XX 11-MAR-1998; 98US-0037990.
XX XX
XX (GALL-) GALLLO WINERY E & J.
XX XX
XX Engel SR, Descenzo RA, Morenzoni RA, Irelan NA;
XX XX
XX WPI: 1999-551425/46.
XX XX
XX New isolated fungal and yeast nucleic acids, used for identifying
XX different fermentation-related microorganisms, particularly in wine
XX fermentation cultures
XX XX
XX Disclosure: Page 32; 52pp; English.
XX XX
XX This is the nucleotide sequence for the Internal Transcribed Spacer
XX (ITS) of P. crustosum. This sequence was amplified directly from the
XX isolate by the ITS5 (AA222530) and ITS4 (22531) primers.
XX XX
XX The invention is directed to the identification of different
XX fermentation related microorganisms, particularly those involved in the
XX production of wine. The invention utilizes a polymerase chain reaction
XX (PCR) based diagnostic assay of DNA sequences located in the Internal
XX Transcribed Spacer (ITS) region of the ribosomal RNA gene.
XX XX
XX Ribosomal genes are suitable for use as molecular probe targets because
XX of their high copy number. Non transcribed and transcribed spacer
XX sequences associated with ribosomal genes are usually poorly conserved
XX and, thus, are advantageously used as target sequences for the detection
XX of recent evolutionary divergence. Fungal rRNA genes are organized in
XX units. Each unit encodes mature subunits of 18S, 5.8S and 28S rRNA. The
XX ITS region lies between the 18S and 28S rRNA genes and contains two
XX variable non-coding spacers (ITS1 and ITS2) and the 5.8S rRNA gene.
XX XX
SO Sequence 498 BP: 93 A; 154 C; 139 G; 112 T; 0 other:

Query Match 60.4%; Score 220.6; DB 20: Length 498;
Best Local Similarity 90.8%; Pred. No. 2.3e-56;
Matches 268; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1 aaacttcaacaatgagatcctctgttcgcgcatcgatgaagaacgacgacatgcgat 60
DB 176 aaacttcaacaatgagatcctctgttcgcgcatcgatgaagaacgacgacatgcgat 235
QY 61 aagtaatgtgaattgagaatcagatcagatcagatcgtttgaaagcagatgcgcc 120
DB 236 aagtaatgtgaattgagaatcagatcagatcagatcgtttgaaagcagatgcgcc 294
QY 121 ctggatctcgggggagcagatcgttcgagcgatcgttcgtccccaagcagcgctgtg 180
DB 295 ctggatctcgggggagcagatcgttcgagcgatcgttcgtccccaagcagcgctgtg 354
QY 181 gtgttggtcgtcgtccccc-cgccccggggagcagcgccgaaagcagcgcgacagc- 238
DB 355 gtgttggtcgtcgtcccccctcccgggggagcagcgccccaagcagcgcgacagc 414
QY 239 tcgggtcctcgagcgatcgagggctgttcacccgctcgttcagcgccgagcgcg 293
DB 415 tcgggtcctcgagcgatcgagggctgttcacccgctcgttcagcgccgagcgcg 469

RESULT 8
AA290111
ID AA290111 standard; DNA: 610 BP.
AC AA290111;
XX XX
XX 17-SEP-1999 (first entry)
XX XX
```

XX Phomopsis viticola (variant 2) Internal transcribed spacer DNA sequence.
 DE ITS1: ITS2: Internal transcribed spacer: detection: fungal pathogen:
 XX grape: ribosomal RNA gene region: Identification: wine: ds.
 KM
 OS Phomopsis viticola.
 XX

PN WO929689-A1.
 XX

PD 17-JUN-1999.
 XX

PF 07-DEC-1998: 98WO-US25210.
 XX

PR 08-DEC-1997: 97US-0986727.
 XX

PA (GALL-) GALLO WINERY E & J.
 XX

PI Descenzo RA, Engel SR, Irelan NA;
 XX

DR WPI: 1999-429921/36.
 XX

PT Novel primers targeted to Internal transcribed spacer region of
 XX fungal pathogen ribosomal DNA genes
 XX

PS Disclosure: Page 32; 43pp; English.
 XX

CC The present invention describes oligonucleotides (I) for identifying
 CC fungal pathogens, especially of grape plants. The oligonucleotides
 CC are isolated double stranded nucleic acids representing the internal
 CC transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the
 CC organisms *Eutypella vitis*, *Eutypa lata*, *Phomopsis viticola* or
 CC *Diplodia gossypina*. The oligonucleotide are used to detect the fungal
 CC pathogens *Eutypella vitis*, *Eutypa lata*, *Phomopsis viticola* or *Diplodia*
 CC *gossypina*, especially when infecting grape plants. The detection method
 CC is used in the wine industry. AAX90075 to AAX90094 represent
 CC specifically claimed oligonucleotides from the present invention.
 CC AAX90095 to AAX90105 represent specifically claimed PCR primers for use
 CC in the detection of the fungal pathogens *Eutypella vitis*, *Eutypa lata*,
 CC *Phomopsis viticola* or *Diplodia gossypina*. The present sequence represents
 CC an ITS DNA sequence from the present invention.
 XX
 XX Sequence 610 BP: 150 A; 175 C; 163 G; 122 T; 0 other:

Query Match 56.7%; Score 206.8; DB 20; Length 610;
 Best Local Similarity 76.8%; Pred. No. 3.3e-52;

Matches 281; Conservative 0; Mismatches 77; Indels 8; Gaps 2;

OY 1 aaacttcaacaatgattctctgttccgcacatgataagaacgacgaactgcgat 60
 |||||||
 DB 232 aaacttcaacaacgagatctctgttccgcacatgataagaacgacgaactgcgat 291
 |||||||
 OY 61 aagtaatgtaatttcagaaatcagtaacatcagatcttgaacgacgaactgcgcccc 120
 |||||||
 DB 292 aagtaatgtaatttcagaaatcagtaacatcagatcttgaacgacgaactgcgcccc 351
 |||||||
 OY 121 ctggcattccgggggagcctgtctcgcagcgtlcatctgctgcacccaagccgggtttg 180
 |||||||
 DB 352 ctggattccggggagcctgtctcgcagcgtlcatctgctgcacccaagccgggtttg 411
 |||||||
 OY 181 tcttgagtgctgcgtcccccgcgggggagcggcccgaaagcagcgcgacacgctc 240
 |||||||
 DB 412 gatggggacactctctcccccgcgggggagcggcccgaaatccagtgcgagctcg 468
 |||||||
 OY 241 cggctctcagcgtatgagggcctgtgcacccgctgattagcgccggcgacgcacgc 300
 |||||||
 DB 469 -----ccaggaaccccgagcagtagtaaacctcgtctcggggaagccctgcggtgccc 524
 |||||||
 OY 301 ggcgttccaaactatctt-tctcaggttgacctcgtacgtaacgtaagatacccgctga 359
 |||||||
 DB 525 tgcggttaaaccccaactctcgaagtttgacctcgtacgtaagatacccgctga 584
 |||||||

OY 360 actta 365
 ||||||
 DB 585 actta 590

RESULT 9

AAV70872
 ID AAV70872 standard; DNA: 309 BP.

AC AAV70872;
 XX

DT 26-FEB-1999 (first entry)
 XX

DE Internal transcribed spacer 2 (ITS2) and adjacent regions.
 XX

Internal transcribed spacer 2: ITS2: probe: *Aspergillus flavus*;
 KM *A. niger*; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*;
 KM *Mucor rouxii*; *M. racemosus*; *M. plumbeus*; *A. fumigatus*;
 KM *M. circinalloides* f. *circinalloides*; *Rhizopus oryzae*; *R. microsporus*;
 KM *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abisida corymbifera*;
 KM *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;
 KM *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.
 XX

OS *Penicillium notatum*.
 XX

PN WO9850584-A2.
 XX

PD 12-NOV-1998.
 XX

PF 01-MAY-1998: 98WO-US08926.
 XX

PR 02-MAY-1997: 97US-0045400.
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX

PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;
 XX

DR WPI: 1999-034737/03.
 XX

PT New nucleic acid probes for filamentous fungi - for detecting e.g.
 PT *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abisida*,
 PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*
 PT species.
 XX

PS Claim 1: Page 19; 45pp; English.
 XX

CC The present sequence represents an internal transcribed spacer 2 (ITS2)
 CC and adjacent regions. Probes can be derived from the present sequence
 CC which are species-specific. The specification also describes ITS2
 CC sequence-derived probes for identifying a species selected from
 CC *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,
 CC *M. indicus*, *M. circinalloides* f. *circinalloides*, *Rhizopus oryzae*,
 CC *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*,
 CC *Abisida corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii*
 CC (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or
 CC *Sporothrix schenckii*. The probes can be used for differentiating
 CC filamentous fungal species from each other and from other medically
 CC important fungi.
 XX

SO Sequence 309 BP: 57 A; 92 C; 91 G; 69 T; 0 other:

Query Match 56.6%; Score 206.6; DB 20; Length 309;
 Best Local Similarity 87.0%; Pred. No. 3e-52;
 Matches 274; Conservative 0; Mismatches 34; Indels 7; Gaps 4;

OY 52 aacgcgataagtaatgtaatttcagaaatcagtaacatcagatcgttgaacgaca 111
 |||||||
 DB 1 aatgcgatacgaatgtaatttcga-aattcagtaacatcagatcgttgaacgaca 59
 |||||||
 OY 112 ttgcgcccccgagcattccgggggagcctgtctcgcagcgtacatctgcacctcaagcc 171
 |||||||

Dd	60	ctgcgccccctggtattccggggggaatgctgtcctcgagcgcatctgtcgccttaagca	119
Oy	172	cgcctgtgtgtgttggatcgtctgcccccgcggggagacggccgaaaggacggcg	231
Oy	173		
Dd	120	cgcctgtgtgtgttggcgccccgtccctccgatcccgggggaacggccgaaggacggcg	179
Oy	232	gcaccg-gtccggtcttcctcgagcgatgtgggctgtgttacccgctcgattggcgccgg	290
Oy	180	gcaccggtctcggtcttcctcgagcgatgtgggctgtgtgtcacccgctc--tgttagcccgcc	237
Dd	291	ggcgccgcgcggcggtctccacaaccttatctttcaggttgaccccgagatcagtagaat	350
Dd	238	ggcgctgtgccgatccaacccaattc---ttaccggtgtgaccccgatacgaagaagt	294
Oy	351	accgcgtgaacttaa	365
Dd	295	accgcgtgaacttaa	309
<hr/>			
RESULT 10			
AAX90112	10	AAX90112 standard; DNA; 568 BP.	
XX		AAX90112:	
XX		17-SEP-1999 (first entry)	
DE		Diplodia gossypina internal transcribed spacer DNA sequence.	
XX		ITS1: ITS2: Internal transcribed spacer; detection: fungal pathogen;	
KW		grape; ribosomal RNA gene region; identification: wine; ds.	
XX		Diplodia gossypina.	
OS		M09292899-A1.	
PN		17-JUN-1999.	
PD		07-DEC-1998: 98MO-US25210.	
XX		08-DEC-1997: 97US-0986727.	
PR		(GALL-) GALLO WINERY E & J.	
PA		Deascenzo RA, Engel SR, Ireilan NA:	
XX		WP1: 1999-429921/36.	
DR		Novel primers targeted to internal transcribed spacer region of	
XX		fungal pathogen ribosomal DNA genes	
PT		Disclosure: Page 32-33; 43pp: English.	
PS		The present invention describes oligonucleotides (I) for identifying	
XX		fungal pathogens, especially of grape plants. The oligonucleotides	
CC		are isolated double stranded nucleic acids representing the internal	
CC		transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the	
CC		organisms Eutypella vitis, Eutypa lata, Phomopsis viticola or	
CC		Diplodia gossypina. The oligonucleotide are used to detect the fungal	
CC		pathogens Eutypella vitis, Eutypa lata, Phomopsis viticola or Diplodia	
CC		gossypina, especially when infecting grape plants. The detection method	
CC		is used in the wine industry. AAX90075 to AAX90094 represent	
CC		specifically claimed oligonucleotides from the present invention.	
CC		AAX90095 to AAX90105 represent specifically claimed PCR primers for use	
CC		in the detection of the fungal pathogens Eutypella vitis, Eutypa lata,	
CC		Phomopsis viticola or Diplodia gossypina. The present sequence represents	
CC		an ITS DNA sequence from the present invention.	
XX		Sequence 568 BP; 142 A; 147 C; 144 G; 135 T; 0 other;	

Query Match	55.8%;	Score 203.8;	DB 20;	Length 568;
Best local Similarity	76.4%;	Pred. No. 2;5e-51;		

	Matches	279, Conservative	0, Mismatches	77, Indels	9, Gaps	2
yy	1	aaacttcaacaatlgatctctctgtgttcgcgcatagaagaacgcagcaactgcgat	60			
bb	191	aaactttcaacaacagcatctctctgtctctgcatacgtagaagcagcagcaaatltgcgt	250			
yy	61	aagtaaatgtgaattgcgcaattcaaggaatcatcaggtctctttgaagcagcatggcccc	120			
bb	251	aagtaaatgtgaattgcgcaattcaaggaatcatcaggtctctttgaagcagcatggcccc	310			
yy	121	ctggcattccggggagatccgctgcgcagcgtcatctgcctccataaagcccgagctgtg	180			
bb	311	tgtgtatccggggggagatccgctgcgcagcgtcatctgcctccataaagcccgagctgtg	368			
yy	181	tgtgtgtgtcgtcgtcccccgc	240			
bb	369	---gaatttggcaccgctctctcactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	424			
yy	241	cggtccctccgcagcgtatggggtctgtgtacccgcgcgtcatgtaggcgcgcgcgcgcgcgc	300			
bb	425	cagccctccaaacgtagatagataataacctgcgtcttggagtggtgtgcgtgcgcgcgcgcgc	484			
yy	301	ggcgtctccaaacttacttctcgaagtttgacctcgcgatcaggtatggatatacccgctgaa	360			
bb	485	gaacctctcgaacttctct---caaggttgacctcgcgatcaggtatggatatacccgctgaa	541			
yy	361	cttaa 365				
bb	542	cttaa 546				

Result	11
AAH73767	
ID	AAH73767 standard; DNA: 640 BP.
XX	
AC	AAH73767;
XX	
DT	08-OCT-2001 (first entry)
XX	
DE	Guignardia citricarpa rRNA gene ITS region, SEQ ID NO:4.
XX	
KW	Ribosomal RNA gene; rRNA gene; Internal transcribed spacer; ITS;
KW	pathogenic; citrus blackspot disease; citrus fruit; differentiation;
KW	characterisation; detection; ds.
XX	
OS	Guignardia citricarpa.
XX	
EH	Key
EH	Location/Qualifiers
FT	1..32
FT	/*tag- a
FT	/partial
FT	/product= "18S ribosomal RNA"
FT	33..266
FT	/*tag- b
FT	/note= "Internal transcribed spacer (ITS) 1"
FT	267..424
FT	/*tag- c
FT	/product= "5.8S ribosomal RNA"
FT	425..589
FT	/*tag- d
FT	/note= "Internal transcribed spacer (ITS) 2"
FT	590..640
FT	/*tag- e
FT	/partial
FT	/product= "28S ribosomal RNA"
XX	
PN	MO20015318-A2.
XX	
PD	26-JUL-2001.
XX	
PF	19-JAN-2001; 2001WO-US01735.
XX	
PR	19-JAN-2000; 2000US-0177013.

```
XX PA (UNOR-) UNIV OREGON.
XX PI Carroll GC;
XX DR WPI: 2001-465362/50.
XX PT New differentiating oligonucleotides which hybridizes with a target DNA
XX PT sequence associated with pathogenic or non-pathogenic species of
XX PT Guignardia, for differentiating pathogenic from non-pathogenic species
XX PT
XX PS Claim 11: Fig 1: 33pp; English.
XX CC The invention relates to oligonucleotide amplification primers and
XX CC methods for the detection of pathogenic Guignardia citricarpa. Guignardia
XX CC citricarpa is a fungus which causes citrus blackspot disease, producing
XX CC progressive black surface lesions on the fruits of most commercial citrus
XX CC cultivars such as oranges, lemons, limes, and grapefruit. Although this
XX CC is a cosmetic disease, it causes significant losses to the citrus fruit
XX CC growing industry, as many countries do not permit the importation of
XX CC affected fruit. However, there is a second, non-pathogenic Guignardia
XX CC species, Guignardia citricarpa, which also infects citrus fruit, but
XX CC which forms insignificant lesions. This non-pathogenic Guignardia species
XX CC is morphologically almost indistinguishable from the pathogenic
XX CC Guignardia citricarpa, and both species may be simultaneously present on
XX CC one fruit. The primers of the invention are targeted to the internal
XX CC transcribed spacer (ITS) regions of the ribosomal RNA gene of either the
XX CC pathogenic Guignardia citricarpa (see AAH73768) or the non-pathogenic
XX CC Guignardia citricarpa (see AAH73768). These regions exhibit significant
XX CC differences between the two species, and provides a means by which the
XX CC two species may be distinguished from one other. The present sequence
XX CC represents the rRNA gene ITS region of the pathogenic Guignardia
XX CC citricarpa.
XX SO Sequence 640 BP; 152 A; 167 C; 169 G; 152 T; 0 other;

Query Match 53.5%; Score 195.2; DB 22; Length 640;
Best Local Similarity 74.7%; Pred. No. 1e-48;
Matches 275; Conservative 0; Mismatches 83; Indels 10; Gaps 2;

OY 1 aaacttcaacatgatactcttggttcggcatcgatgaagaacgagcaactcgcat 60
DB 267 aaacttcaacacgcatctcttggttcggcatcgatgaagaacgagcaactcgcat 326
OY 61 aagtaatgtgaattcagaatcaatgaatcatcgatcgatcttgaacgacattcgccac 120
DB 327 aagtaatgtgaattcagaatcaatgaatcatcgatcgatcttgaacgacattcgccac 386
OY 121 ctggcattccgggggacatgacctgctcagagcgatcatgctccctcaagccggcttg 180
DB 387 ctggcattccgggggacatgacctgctcagagcgatcatgctccctcaagccgtcttg 446
OY 181 tgttgggtcgtgctcccccgggggagcgagccgaaagcgagcgagccagctc 240
DB 447 attgg-----gagcagctccgctgacgagcgagccgagcaactcggcgagcgctc 499
OY 241 cggctccgagcgatctgggcttggttcacccgctcgatgaaggccggcgagccagcc 300
DB 500 cggctccgagcgatctgggcttggttcacccgctcgatgaaggcgagcgctgagccgagc 559
OY 301 ---ggcgtcccaacctatctctcaggtgagccctcgatcaggtagggataccgct 357
DB 560 aatcgacctcgatcattcttccaaaggtgacctcgatcaggtagggataccgct 619
OY 358 gaacttaa 365
DB 620 gaacttaa 627
```

RESULT 12
AAx90110

```
ID AAX90110 standard; DNA; 608 BP.
XX AC AAX90110;
XX DT 17-SEP-1999 (first entry)
XX DE Phomopsis viticola (variant 1) Internal transcribed spacer DNA sequence.
XX KM ITS1; ITS2: Internal transcribed spacer; detection; fungal pathogen;
XX KM grape; ribosomal RNA gene region; identification; wine; ds.
XX OS Phomopsis viticola.
XX PN MO9929899-AL.
XX PD 17-JUN-1999.
XX PF 07-DEC-1998; 98MO-US25210.
XX PR 08-DEC-1997; 97US-0986727.
XX PA (GALL-) GALLO WINERY E & J.
XX PI Descenzo RA, Engel SR, Ireland NA;
XX DR WPI: 1999-429921/36.
XX PT Novel primers targeted to internal transcribed spacer region of
XX PT fungal pathogen ribosomal DNA genes
XX PS Disclosure; Page 31; 43pp; English.
XX CC The present invention describes oligonucleotides (I) for identifying
XX CC fungal pathogens, especially of grape plants. The oligonucleotides
XX CC are isolated double stranded nucleic acids representing the internal
XX CC transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the
XX CC organisms Eutypella vitis, Eutypa lata, Phomopsis viticola or
XX CC Diplodia gossypina. The oligonucleotide are used to detect the fungal
XX CC pathogens Eutypella vitis, Eutypa lata, Phomopsis viticola or Diplodia
XX CC gossypina, especially when infecting grape plants. The detection method
XX CC is used in the wine industry. AAX90075 to AAX90094 represent
XX CC specifically claimed oligonucleotides from the present invention.
XX CC AAX90095 to AAX90105 represent specifically claimed PCR primers for use
XX CC in the detection of the fungal pathogens Eutypella vitis, Eutypa lata,
XX CC Phomopsis viticola or Diplodia gossypina. The present sequence represents
XX CC an ITS DNA sequence from the present invention.
XX SO Sequence 608 BP; 154 A; 166 C; 153 G; 135 T; 0 other;

Query Match 51.6%; Score 188.4; DB 20; Length 608;
Best Local Similarity 75.4%; Pred. No. 1.e-46;
Matches 276; Conservative 0; Mismatches 81; Indels 9; Gaps 3;

OY 1 aaacttcaacatgatactcttggttcggcatcgatgaagaacgagcaactcgcat 60
DB 231 aaacttcaacacgcatctcttggttcggcatcgatgaagaacgagcaactcgcat 290
OY 61 aagtaatgtgaattcagaatcaatgaatcatcgatcgatcttgaacgacattcgccac 120
DB 291 aagtaatgtgaattcagaatcaatgaatcatcgatcgatcttgaacgacattcgccac 350
OY 121 ctggcattccgggggacatgacctgctcagagcgatcatgctccctcaagccggcttg 180
DB 351 ctggcattccgggggacatgacctgctcagagcgatcatgctccctcaagccgttgctg 409
OY 181 tgttgggtcgtgctcccccgggggagcgagccgaaagcgagcgagccagctc 240
DB 410 tgaatgggacctcttcttccaaagagcagcgccgtaaatcaatgagtgagctg--- 466
OY 241 cggctccgagcgatctgggcttggttcacccgctcgatgaaggcgagcgagccagcc 300
DB 467 -----ccagagcccgagcgagcagtaagtaaacctcgtctcggaagcgcttgagctgcc 522
```

[illegible]

CC affected fruit. However, there is a second, non-pathogenic *Gulgnardia*
CC species, *Gulgnardia citricarpa*, which also infects citrus fruit, but
CC which forms insignificant lesions. This non-pathogenic *Gulgnardia* species
CC is morphologically almost indistinguishable from the pathogenic
CC *Gulgnardia citricarpa*, and both species may be simultaneously present on
CC one fruit. The primers of the invention are targeted to the internal
CC transcribed spacer (ITS) regions of the ribosomal RNA gene of either the
CC pathogenic *Gulgnardia citricarpa* (see AAH73767) or the non-pathogenic
CC *Gulgnardia citricarpa* (see AAH73768). These regions exhibit significant
CC differences between the two species, and provides a means by which the
CC two species may be distinguished from one other. The present sequence
CC represents the rRNA gene ITS region of the non-pathogenic *Gulgnardia*
CC *citricarpa*.

XX
SQ Sequence 618 BP; 146 A; 159 C; 155 G; 158 T; 0 other;

Query Match	Similarity	50.4%	Score	184;	DB	22:	Length	618:	
Best Local	Similarity	73.1%	Pred.	No. 2.2e-45:					
Matches	266:	Conservative	0:	Mismatches	90:	Indels	8:	Gaps	2:
Oy	1	aactcttcacaatgatactccttgytlccgcgatcgatatgaagaacgcagcaactgcgat	60						
Db	262	aaactcttcacaacgatattcttggtlctgcgatcgatgaagaacgcagcaaatggcat	321						
Oy	61	aagtaattgtaattgcagaattcagaatcagatcgagttcttgaaccgacattgcgcc	120						
Db	322	aagtaattgtaattgcagaattcagaatcagatcgaattcttgaaccgacattgcgcc	381						
Oy	121	cgcgcattccggagggcagcgcctgtctcgcagcgtcatgtctgtcccttaaacccgcgctgtg	180						
Db	382	cgcgcattccggagggcagcgcctgtctcgcagcgtcatattcaaccttaaacctctgtctgtg	441						
Oy	181	tgttggatcgtcgtcccccccggaggagcggccgaagcagcggcggcagccgttc	240						
Db	442	attgg-----gcaacgltccgctgcgcggacgttccctgaagaccctcggcagcgtcc	494						
Oy	241	cgttcctcgagcgtataggcgttgytccaccgcgtcgattaggcgcggccgggcgcag-c	299						
Db	495	tgcctcgcagcgtataggaaataatctcgtcttggagtgcctgggcgcagcgcgcgcgcgac	554						
Oy	300	cggcgtctccaaccttatcttcttcaggltgcacctgcagatcagatcagatccgcgtga	359						
Db	555	aatcgaccttcgtcatatttcccaaagltgcacctgcagatcagatcagatccgcgtga	614						
Oy	360	acct 363							
Db	615	acct 618							
<hr/>									
RESULT 14									
AAV43265									
ID	AAV43265	standard:	DNA;	597	Bp.				
XX	XX								
AC	AAV43265;								
XX	XX								
DT	26-OCT-1998	(first entry)							
XX	XX								
DE	Sequence of ITS region from Kabatiella zeae, isolate 56351.								
XX	XX								
KM	Internal transcribed spacer; ITS; detection; maize; fungal pathogen; ss.								
XX	XX								
OS	Kabatiella zeae.								
XX	XX								
FH	Key	Location/Qualifiers							
FT	misc_feature	1..30							
FT	FT	/tag= "a							
FT	FT	/note= "3' end of small subunit rRNA gene"							
FT	FT	31..217							
FT	FT	/tag= "b							
FT	FT	/note= "ITS1"							
FT	FT	218..373							
FT	FT	/tag= "C							

Db 361 ggcgttgaggatcgctctgcctlmvgcgcgtgcgcgcgcgcgaalatcatlgtgcgtctc 420
Oy 237 ggtccggtctctgaggtatgaggcttggtcacccgctcgattaggccgcgggcgcgc 296
Db 421 g-----ctgcagccctccatlgcgtagtaagctaaacctcgcaactggaacgcggcgc 472
Oy 297 agccgcgtctccaacttatcttctcaggttgacctcgatcaggtagggataaccgcgc 356
Db 473 ggcctagcgttaaaccccaactctcgaatgttgacctcgatcaggtaggaataaccgcgc 532
Oy 357 tgaacttaa 365
Db 533 tgaacttaa 541

Search completed: August 21, 2002, 22:22:38
Job time: 5778 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 18:03:41 ; Search time 5019.06 Seconds

(without alignments)
981.536 Million cell updates/sec

Title: US-10-046-955-5
Perfect score: 365
Sequence: 1 aaacttcaacatgatct.....gggatacccgctgaactaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
C 1	230	63.0	318 9	AI213025 Y6f01a1.f
C 2	188	51.5	213 9	AI209736 C7G08a1.f
3	178.8	49.0	227 9	AA965960 r8a05a1.r
4	149.2	40.9	189 9	AA783772 C7G08a1.r
5	143.8	39.4	882 12	CNS06XIS
6	142.2	39.0	1117 12	CNS07ARF
C 7	141.4	38.7	718 12	CNS06FTN
C 8	141.4	38.7	827 12	CNS06FMV
C 9	141.4	38.7	866 12	CNS06FVF
C 10	141.4	38.7	869 12	CNS06DGL
C 11	141.4	38.7	889 12	CNS06DHL
12	141.4	38.7	902 12	CNS06CUX
13	141.4	38.7	928 12	CNS06FUG
C 14	141.4	38.7	936 12	CNS06CB4
15	141.4	38.7	960 12	CNS06FXB
16	141.4	38.7	962 12	CNS06F02
C 17	141.4	38.7	1000 12	CNS06FNV

18	141.4	38.7	1006 12	CNS06CYX	AL393152 T3 end of
C 19	141.4	38.7	1625 12	CNS06DA6	AL393556 T3 end of
20	141.4	38.7	1036 12	CNS06DOL	AL394147 T7 end of
21	141.4	38.7	1045 12	CNS06CNZ	AL392757 T3 end of
22	141.4	38.7	1048 12	CNS06CN3	AL392725 T3 end of
23	140	38.4	141 9	AI327879	AI327879 j0906a1.r
24	139.4	38.2	448 12	A2916873	A2916873 4911.f463
25	139.4	38.2	885 12	CNS06HJY	AL399092 T3 end of
C 26	139.4	38.2	922 12	CNS06HOU	AL399268 T7 end of
27	139.4	38.2	938 12	CNS06HIO	AL399046 T7 end of
28	139.4	38.2	943 12	CNS06H40	AL399814 T7 end of
29	139.4	38.2	950 12	CNS06JAK	AL401346 T3 end of
C 30	139.4	38.2	953 12	CNS06GAR	AL397249 T3 end of
C 31	139.4	38.2	961 12	CNS06HT1	AL399419 T7 end of
C 32	139.4	38.2	962 12	CNS06G9U	AL397432 T3 end of
C 33	139.4	38.2	963 12	CNS06JVG	AL401198 T7 end of
C 34	139.4	38.2	966 12	CNS06H1T	AL399735 T3 end of
C 35	139.4	38.2	977 12	CNS06J9K	AL401310 T3 end of
C 36	139.4	38.2	982 12	CNS06HM6	AL399172 T3 end of
37	139.4	38.2	985 12	CNS06JLS	AL401750 T3 end of
C 38	139.4	38.2	997 12	CNS06HOW	AL399342 T3 end of
C 39	139.4	38.2	1024 12	CNS06H7C	AL398638 T3 end of
C 40	139.4	38.2	1035 12	CNS06JNU	AL401813 T3 end of
41	139.2	38.1	214 10	BF251183	BF251183 EST418443
C 42	139	38.1	360 12	A2923094	A2923094 4908.9e87
C 43	139	38.1	424 12	A2923253	A2923253 4908.f420
44	139	38.1	456 12	A2923320	A2923320 4908.f420
C 45	139	38.1	481 12	A0491983	A0491983 V11612 m

ALIGNMENTS

RESULT 1
AI213025/c 318 bp mRNA linear EST 19-OCT-1998
Y6f01a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emricella nidulans cDNA clone
Y6f01a1 3', mRNA sequence.

ACCESSION AI213025.1 GI:3774967
VERSION AI213025.1
KEYWORDS EST.
SOURCE Emricella nidulans.
ORGANISM Emricella nidulans
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emricella.
AUTHORS Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
Prade, R. and Roe, B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other-ESTs: Y6f01a1.f1
Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 265.
Location/Qualifiers
1..318
/organism="Emricella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="Y6f01a1"
/clone_1b="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

FEATURES

source

XhoI, 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript*

BASE COUNT 69 a 93 c 88 g 68 t

ORIGIN

Query Match 63.0%; Score 230; DB 9; Length 318;
Best Local Similarity 98.4%; Pred. No. 1.3e-46;
Matches 254; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgagatctctgtgtccgcatcagatgaagaacgacgacatgcgat 60
DB 255 AAACCTTCAACAATGAGATCTCTGTCCGCAATCATGAAACGACGACGAACTCGAT 196
OY 61 aagtaatgtaatttgcgaatttcagtgaatcatcagatctttaaagacatctgcaccc 120
DB 195 AAGTAATGTAATTCAGATTCAGTGAATCATGAGATCTTGAAGCAGCATTTGCCCCC 136
OY 121 ctggcattccgggggacatgcctgcagagcgatcgtctgcctcaagccgagctgtg 180
DB 135 CTGGCATTCGGGGGGGATCGTCCGAGCGTCATTGGTCCCTCAAGCCGCGTTGG 76
OY 181 tgttggt 239
DB 75 TGTGGGTCTCTGCT---CCGCCCGGGGAGCGGCCGAAAGGACGCGCGCATCCGTGT 19
OY 240 ccggtccctcagcgatg 257
DB 18 CCGGTCTCTCAGCGCTATG 1

RESULT 2
AI209736/c 213 bp mRNA linear EST 19-OCT-1998
LOCUS
DEFINITION c7g08a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
c7g08a1.3', mRNA sequence.
ACCESSION AI209736 GI:3771678
VERSION AI209736
KEYWORDS EST.
SOURCE Emericella nidulans.
ORGANISM Emericella nidulans.
REFERENCE Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
AUTHORS 1 (bases 1 to 213)
Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: c7g08a1.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20.

FEATURES

source Location/Qualifiers
1..213
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="c7g08a1"

/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 43 a 68 c 63 g 39 t

ORIGIN

Query Match 51.5%; Score 188; DB 9; Length 213;
Best Local Similarity 98.1%; Pred. No. 2.5e-36;
Matches 212; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

OY 41 agaagcgcggaactgcgataagtaatgtaatgcgaattcagatcagatcagatc 100
DB 213 AAGAGCGGCGGAACTGCATTAATGTGAATTCAGAAATTCAGTGAATCATGAGTCT 154
OY 101 ttgaagcagcatttggcccccctgcagtcgaggggacatgccttcagagcattgct 160
DB 133 TTGAACGACATTCGCGCCCTCGCATTCGCGGGGACATGCTTCCAGCGCTATTGCT 94
OY 161 gccctcaagcccggt 220
DB 93 GCCCTCAAGCCCGGCTGTGTGTGGTGTGTCGT---CCCCCGGGGAGCGGCCGAA 37
OY 221 aggcagcgcggaacg-gtccggtccctcagagcta 255
DB 36 AGCGAGCGGCGCACCGTCTCGCTCGAGCGTA 1

RESULT 3
AA965960 227 bp mRNA linear EST 31-JUL-1998
LOCUS
DEFINITION r8a05a1.r1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
r8a05a1.5', mRNA sequence.
ACCESSION AA965960
VERSION AA965960
KEYWORDS EST.
SOURCE Emericella nidulans.
ORGANISM Emericella nidulans.
REFERENCE Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
AUTHORS 1 (bases 1 to 227)
Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: SK
High quality sequence stop: 153.

FEATURES

source

Location/Qualifiers
1..227
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="r8a05a1"

/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 40 a 65 c 74 g 48 t

ORIGIN

Query Match 49.0%; Score 178.8; DB 9; Length 227;
Best Local Similarity 94.8%; Pred. No. 4.6e-34;
Matches 218; Conservative 0; Mismatches 7; Indels 5; Gaps 3;

[illegible]

LOCUS	189 bp	mRNA	linear	EST 29-JUL-1998
AA783772				
C790861.1	Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone C790861.5', mRNA sequence.			

ACCESSION	AA783772	
VERSION	AA783772.1	GI:2843940
KEYWORDS	EST.	
SOURCE	Emeritella nidulans.	
ORGANISM	Emeritella nidulans	

REFERENCE
AUTHORS
Eumariota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emmentella.
1 (bases 1 to 189)
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,

TITLE Prade, R. and Roe, B.
An *Aspergillus nidulans* EST Database
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Dept. of Chemistry and Molecular Biology

Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
 Seq primer: SK.

FEATURES	Location/Qualifiers
source	1. .189

BASE COUNT	ORIGIN
32 a	1 others
61 c	54 g
54 g	41 t
41 t	3' end of CDNA cloned into XhoI site of pBluescript
3' end of CDNA cloned into XhoI site of pBluescript	
	note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
	XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript
	developmental and vegetative mycelia, asexual structures"
	/clone="c7g08a1"
	/db_xref="taxon:162425"
	/strain="FGSC A26"
	/organism="Emmericella nidulans"
	/clone_lib="Aspergillus nidulans 24hr asexual

Query Match	40.9%	Score 149.2;	DB 9;	Length 189;
Best Local Similarity	93.2%;	Pred. 8.4e-27;		
Matches 178: Conservative	0;	Mismatches 9;	Indels 4;	Gaps 2;

Oy 67 tgtgaattgcagaatctcagtcgatacatcgagtctttgaacgcacatttgcgcccttgca 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ttctgaattgcAAAATTCAGTGAATCATCATCTTTGSAACGCACATTGGCCCCCCTGGCA 60

QY 127 ttccggggggcatgcctcgttccgagcgtcatctgctgcctccaagcccgctgtgtgtgg 186
|||||
Db 61 ttccgggggggcattgccttccgagcgtcatctgctgcctccaagcccgctgtgtgtgg 120
|||||

[illegible]

RESULT	5
CNS06XIS	
LOCUS	882 bp DNA
DEFINITION	linear GSS 06-JUL-2001
ACCESSION	U7 end of clone AY0A001C10 of library AY0A from strain CBS 6340
VERSION	of Kluyveromyces thermotolerans, genomic survey sequence.
KEYWORDS	AL419786
	AL419786.1 GI:1202964
	GSS.

SOURCE	ORGANISM	REFERENCE	AUTHORS
Kluyveromyces thermotolerans.	Kluyveromyces thermotolerans		
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.			
1 (bases 1 to 882)			
Malpertuy, A., Llorente, B., Blandin, G., Artiguenave, F., Wincker, P.			

TITLE	and Dujon, B. Genomic exploration of the hemiascomycetous yeasts: 10. Kluyveromyces thermotolerans
JOURNAL	FEBS Lett. 487 (1), 61-65 (2000)
MEDLINE	20584720

REFERENCE	AUTHORS	TITLE
2 (bases 1 to 882)	Souchet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., De-Montigny, J., Dujon, B., Durren, P., Lepingle, A., Llorente, B., Malpertuy, A., Neugeglise, C., Ozler-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nicche, C., Wesolowski-Jouvel, M., Wincker, P. and Weissenbach, J.	Genomic exploration of the <i>hemicomycetous</i> yeasts: 1. A set of

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
3 (bases 1 to 882)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvorum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluveromyces thermotolerans*, *Kluveromyces lactis* var. *lactis*, *Kluveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES			
source	location/qualifiers		
	1. .882		
	/organism="Kluyveromyces thermotolerans"		
	/strain="CHS 6340"		
	/db_xref="taxon:4916"		
	/clone="AY0AA001C10"		
	/clone_1lb="AY0AA"		
	/note="end : T7"		
misc-feature	<1. .>882		
	/note="part of rDNA repeats"		
BASE COUNT	/evidence="not_experimental"		
ORIGIN	221 a 188 c 213 g 257 t		3 others

Query Match	39.4%	Score 143.8	DB 12	Length 882
Best Local Similarity	83.6%	Pred. No. 2.4e-25		
Matches 163	Conservative	0	Mismatches 32	Indels 0
				Gaps 0

RESULT	6	CNS07ARF/c	1117 bp	DNA	linear	GSS 08-JUL-2001
LOCUS	DEFINITION	T3 end of clone BC0AA006C06 of library BC0AA from strain CBS 767 of Debaryomyces hansenii, genomic survey sequence.				
ACCESSION	VERSION	AL36945				
KEYWORDS	KEYWORDS	AL36945.1 GI:12220358				
SOURCE	ORGANISM	GSS. Debaryomyces hansenii. Debaryomyces hansenii. Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.				
REFERENCE	AUTHORS	1 (bases 1 to 1117) Ledingle, A., Casaregola, S., Neuveglise, C., Bon, E., Nguyen, H., Artiguenave, F., Wincker, P. and Galliard, C. Genomic exploration of the hemiascomycetous yeasts: 14. Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)				
TITLE	JOURNAL	2 (bases 1 to 1117) Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Boivin, P., Bouteiller, P., Brothier, P., Casaregola, S., de Montigny, J., Dujon, B., Durieux, P., Ledingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Lalonde, O., Potier, S., Saurin, M., Tekala, F., Toftano, N., Lloche, C., Wesolowski, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)				
JOURNAL	MEDLINE	20584711				
REFERENCE	AUTHORS	3 (bases 1 to 1117) Genoscope. Direct Submission Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.				
COMMENT	JOURNAL	1. 1117 location/qualifiers /organism="Debaryomyces hansenii" /strain="CBS 767" /variant="hansenii" /db_xref="taxon:4959" /clone="BC0AA006C06" /clone_lib="BC0AA" /note="end : T3"				
FEATURES	SOURCE					

misc_feature	<1..>1117	/note="part of rDNA repeats"
BASE COUNT	344 a 256 c 204 g 308 t	5 others
ORIGIN		
Query Match	39.0%: Score 142.2; DB 12; Length 1117;	
Best Local Similarity	83.1%: Pred. No. 6.2e-25;	
Matches 162; Conservative	0; Mismatches 33; Indels	0; Gaps 0;
OY	1 aaacttcaacaatgagatcctctgtgtccgagcatgatgaagaaacgcagcgaactgcgat 60	
DB	630 AAACCTTTTCAACAACGAGCATCTCTGGTCTCCGATCATGATGAAGAAGCAGCAAAATGCGAT 571	
OY	61 aagtaatgtaattgcagaattcagtgatcatcatgagatgagctttgaacgcaattgcgccc 120	
DB	570 AAGTAATATGAATTCACATTTTCTGTGATATCATCAAACTTTGAACGCACATTCGCCCT 511	
OY	121 ctgcgcatccg999gagcatcgtctgcagcagtcatactgtcgtccctcaagcccgcttg 180	
DB	510 CTGGATATTCAGAGGCGCATGCGCTGTTAGCGGTATTTCTCTCTCAAACTTCGGGTTGG 451	
OY	181 tgttggtcgtcgtcgc 195	
DB	450 TATTAGTGATATCTC 436	
RESULT 7		
CNS06FTN/c	718 bp	DNA
LOCUS	DEFINITION	T7 end of clone XAR0A001B02 of library XAR0A from strain CBS 732
ACCESSION	AL396849	
VERSION	AL396849.1	GI:12149257
KEYWORDS	GSS.	
SOURCE	Zygosaccharomyces rouxii.	
ORGANISM	Zygosaccharomyces rouxii.	
REFERENCE	1 (bases 1 to 718)	
AUTHORS	de Montigny J., Straub M., Potier S., Tekala F., Dujon B., Wincker P., Artiguenave F. and Souciet J.	
TITLE	Genomic exploration of the hemiascomycetous yeasts: 8.	
JOURNAL	Zygosaccharomyces rouxii	
MEDLINE	FEBS Lett. 487 (1), 52-55 (2000)	
REFERENCE	20584718	
AUTHORS	2 (bases 1 to 718)	
TITLE	Souciet J.L., Aigle M., Artiguenave F., Blandin G., Bojotin-Fukuhara M., Bon E., Brottier P., Casaregola S., de Montigny J., Dujon B., Durrens P., Lepingle A., Llorente B., Malpertuy A., Neuvéglise C., Ozler-Kalogropoulos O., Potier S., Saurin M., Tekala F., Toffano-Nioche C., Wesolowski-Louvel M., Wincker P. and Weissenbach J.	
JOURNAL	Genomic exploration of the hemiascomycetous yeasts: 1. A set of	
MEDLINE	FEBS Lett. 487 (1), 3-12 (2000)	
REFERENCE	20584711	
AUTHORS	3 (bases 1 to 718)	
TITLE	Genoscope.	
JOURNAL	Direct Submission	
COMMENT	Submitted (06-Sep-2000) Genoscope - Centre National de Séquençage. 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marianus var. marianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of	

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremlieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
the other extremity of this insert.
FEATURES
Location/Qualifiers
source
1..866
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0A001E05"
/clone_11b="AR0A"
/note="end : T3"
misc_feature
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence=not_experimental
BASE COUNT 223 a 230 c 166 g 244 t 3 others
ORIGIN
Query Match 38.7%: Score 141.4; DB 12; Length 866;
Best Local Similarity 93.1%: Pred. No. 9.3e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1 aaacttcaacaatgactctctgtgtccgcagatgaagaacgcaggaactgcgat 60
DB 845 AAACCTTCAACACGACGATCTGTGTTCCGATCATGATGAAGAACGACGATCGCAT 786
OY 61 aagtaatgtaattgcagaatcagatcagatcagatcagatcagatcagatcagatc 120
DB 785 ACGTAATGTAATTCGAGATTCGTAATCATGATCTTTGAACGACGATTCGCCGCC 726
OY 121 ctgcgattccgggggagcagtcgtcgcagcgtcatcgc 159
DB 725 TTGCTATTCCGGGGGCGCATGCTGTTGAGCGCATTTTC 687
RESULT 10 869 bp DNA linear GSS 17-JUN-2001
CNS06DGL/ 73 end of clone AR0A013B03 of library AR0A from strain CBS 732 of
LOCUS Zygosaccharomyces rouxii, genomic survey sequence.
DEFINITION
ACCESSION AL393787.1 GI:12144287
VERSION
KEYWORDS GSS.
SOURCE Zygosaccharomyces rouxii.
ORGANISM Zygosaccharomyces rouxii.
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
1 (bases 1 to 869)
TITLE de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souclet,J.
JOURNAL Genomic exploration of the hemiascomycetous yeasts: 8.
MEDLINE Zygosaccharomyces rouxii
REFERENCE FEBS Lett. 487 (1), 52-55 (2000)
20584718
2 (bases 1 to 869)
AUTHORS Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Biolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de Montigny,J., Dujon,B., Durrans,P., Leplingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of

JOURNAL yeast species for molecular evolution studies
MEDLINE FEBS Lett. 487 (1), 3-12 (2000)
REFERENCE 20584711
AUTHORS 3 (bases 1 to 869)
TITLE Direct Submission
JOURNAL Genoscope.
COMMENT Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremlieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
the other extremity of this insert.
FEATURES
Location/Qualifiers
source
1..869
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0A013B03"
/clone_11b="AR0A"
/note="end : T3"
misc_feature
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence=not_experimental
BASE COUNT 242 a 216 c 185 g 226 t
ORIGIN
Query Match 39.7%: Score 141.4; DB 12; Length 869;
Best Local Similarity 93.1%: Pred. No. 9.4e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1 aaacttcaacaatgactctctgtgtccgcagatgaagaacgcaggaactgcgat 60
DB 648 AAACCTTCAACACGACGATCTGTGTTCCGATCATGATGAAGAACGACGATCGCAT 589
OY 61 aagtaatgtaattgcagaatcagatcagatcagatcagatcagatcagatcagatc 120
DB 588 ACGTAATGTAATTCGAGATTCGTAATCATGATCTTTGAACGACGATTCGCCGCC 529
OY 121 ctgcgattccgggggagcagtcgtcgcagcgtcatcgc 159
DB 528 TTGCTATTCCGGGGGCGCATGCTGTTGAGCGCATTTTC 490
RESULT 11 889 bp DNA linear GSS 17-JUN-2001
CNS06DHH/ 73 end of clone AR0A013D02 of library AR0A from strain CBS 732 of
LOCUS Zygosaccharomyces rouxii, genomic survey sequence.
DEFINITION
ACCESSION AL393819.1 GI:12144343
VERSION
KEYWORDS GSS.
SOURCE Zygosaccharomyces rouxii.
ORGANISM Zygosaccharomyces rouxii.
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
1 (bases 1 to 889)
TITLE de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souclet,J.
JOURNAL Genomic exploration of the hemiascomycetous yeasts: 8.
MEDLINE Zygosaccharomyces rouxii
REFERENCE FEBS Lett. 487 (1), 52-55 (2000)
20584718
2 (bases 1 to 889)
AUTHORS Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

TITLE Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveglisse,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 889)

AUTHORS Genoscope.

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
 1..889
 /organism="Zygosaccharomyces rouxii"
 /strain="CBS 732"
 /db_xref="taxon:4956"
 /clone="ARO0A013D02"
 /clone_1lb="ARO0A"
 /note="end : T3"
 /note="end : T3"
 <1..>889
 /note="part of rDNA repeats
 contains 35S rDNA gene"
 /evidence="not_experimental"

BASE COUNT 247 a 222 c 186 g 234 t

ORIGIN

Query Match 38.7%; Score 141.4; DB 12; Length 889;
Best Local Similarity 93.1%; Pred. No. 9.4e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctctctggttcggcatcgatgaagaacgacgcaactgcgat 60
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 648 AAACCTTCAACACGACGATCTCTGTTCTCGCATGTAAGAACGACGACATGCGAT 589
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
QY 61 aagtaatgtaattgcgaattcagatcagatcagatcagatcagatcagatcagatc 120
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
DB 588 ACCTTAATGTGAATTGCGAATTCGTTGATCGAATCGAATCTTTGAACGACATTCGCCGCC 529
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
QY 121 ctggcattccgggggcatgctgctgcagcagcagcagcagcagcagcagcagcagc 159
 ||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
DB 528 TTGGTATTCCGGGGGCGCATGCTGTTTGACGCTCATTTTC 490

RESULT 12
CNS06CUX 902 bp DNA linear GSS 14-JUN-2001
LOCUS T7 end of clone ARO0A008C01 of library ARO0A from strain CBS 732 of
DEFINITION *Zygosaccharomyces rouxii*, genomic survey sequence.
ACCESSION AL393007
VERSION AL393007.1 GI:12142879
KEYWORDS GSS.
SOURCE *Zygosaccharomyces rouxii*.
ORGANISM *Zygosaccharomyces rouxii*.
REFERENCE 1 (bases 1 to 902)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Soulet,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 902)
AUTHORS Soulet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveglisse,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 902)

AUTHORS Genoscope.

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
 1..902
 /organism="Zygosaccharomyces rouxii"
 /strain="CBS 732"
 /db_xref="taxon:4956"
 /clone="ARO0A008C01"
 /clone_1lb="ARO0A"
 /note="end : T7"
 /note="end : T7"
 <1..>902
 /note="part of rDNA repeats
 contains 35S rDNA gene"
 /evidence="not_experimental"

BASE COUNT 236 a 191 c 220 g 254 t 1 others

ORIGIN

Query Match 38.7%; Score 141.4; DB 12; Length 902;
Best Local Similarity 93.1%; Pred. No. 9.4e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctctctggttcggcatcgatgaagaacgacgcaactgcgat 60
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
DB 226 AAACCTTCAACACGACGATCTCTGTTCTCGCATGTAAGAACGACGACATGCGAT 285
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
QY 61 aagtaatgtaattgcgaattcagatcagatcagatcagatcagatcagatcagatc 120
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
DB 286 ACCTTAATGTGAATTGCGAATTCGTTGATCGAATCGAATCTTTGAACGACATTCGCCGCC 345
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
QY 121 ctggcattccgggggcatgctgctgcagcagcagcagcagcagcagcagcagcagc 159
 ||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
DB 346 TTGGTATTCCGGGGGCGCATGCTGTTTGACGCTCATTTTC 384

RESULT 13
CNS06FUG 928 bp DNA linear GSS 17-JUN-2001
LOCUS T7 end of clone XAR0A001C01 of library XAR0A from strain CBS 732
DEFINITION *Zygosaccharomyces rouxii*, genomic survey sequence.
ACCESSION AL396868
VERSION AL396868.1 GI:12149277
KEYWORDS GSS.
SOURCE *Zygosaccharomyces rouxii*.

ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

REFERENCE 1 (bases 1 to 928)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 928)
AUTHORS Souciet,J.L., Algile,M., Artiguenave,F., Blandin,G.,
Boitlin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 928)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE 4
AUTHORS This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source 1..928
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="XAR0A001C01"
/clone_1lb="XAR0A"
/note="end : T7"
/note="end : T7"
misc_feature <1..>928
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence-not_experimental
BASE COUNT 251 a 187 c 230 g 258 t 2 others
ORIGIN

Query Match 38.7%: Score 141.4; DB 12; Length 928;
Best Local Similarity 93.1%: Pred. No. 9.5e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctcttggttcggcatcgatgaagaacgacgaactgcgat 60
|||||
DB 152 AAACCTTCAACAACGATCTCTGTTCTCGCATGATGAAGAACGACGAACGTCGAT 211
|||||
QY 61 aagtaatgtaattgcgaatcagtaatcagatcagtccttgaacgacatggcccc 120
|||||
DB 212 ACCTAATGTGAATTCGCAATTCCTGTAATCATCGAATCTTTGAACGACATTTGGCCCC 271
|||||
QY 121 ctggcatccgggggacatgcctgcgcagacgcatcgc 159
|||||
DB 272 TTGGATTTCGGGGGCGCATGCTGTTTGAAGCGCATTTTC 310
|||||

RESULT 14
CNS06CB4/C
LOCUS CNS06CB4 936 bp DNA linear GSS 14-JUN-2001

DEFINITION T3 end of clone AR0A003E10 of library AR0A from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL392294
VERSION AL392294.1 GI:12141507
KEYWORDS GSS.
SOURCE Zygosaccharomyces rouxii.
ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

REFERENCE 1 (bases 1 to 936)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 936)
AUTHORS Souciet,J.L., Algile,M., Artiguenave,F., Blandin,G.,
Boitlin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 936)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE 4
AUTHORS This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source 1..936
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0A003E10"
/clone_1lb="AR0A"
/note="end : T3"
/note="end : T3"
misc_feature <1..>936
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence-not_experimental
BASE COUNT 266 a 227 c 188 g 245 t 10 others
ORIGIN

Query Match 38.7%: Score 141.4; DB 12; Length 936;
Best Local Similarity 93.1%: Pred. No. 9.5e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctcttggttcggcatcgatgaagaacgacgaactgcgat 60
|||||
DB 649 AAACCTTCAACAACGATCTCTGTTCTCGCATGATGAAGAACGACGAACGTCGAT 590
|||||
QY 61 aagtaatgtaattgcgaatcagtaatcagatcagtccttgaacgacatggcccc 120
|||||
DB 589 ACCTAATGTGAATTCGCAATTCCTGTAATCATCGAATCTTTGAACGACATTTGGCCCC 530
|||||
QY 121 ctggcatccgggggacatgcctgcgcagacgcatcgc 159
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 20:37:27 ; Search time 138.45 Seconds
(without alignments)
647.571 Million cell updates/sec

Title: US-10-046-955-5
Perfect score: 365
Sequence: 1 aaattccacaacatgctc.....gggataccgcgtaactaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	70.1	556	4 US-09-037-9908-7	Sequence 7, Appl
2	220.6	60.4	498	4 US-09-037-9908-6	Sequence 6, Appl
3	206.8	56.7	611	3 US-08-986-727-4	Sequence 4, Appl
4	203.8	55.8	568	3 US-08-986-727-5	Sequence 5, Appl
5	188.4	51.6	608	3 US-08-986-727-3	Sequence 3, Appl
6	180.6	49.5	597	1 US-08-742-023-3	Sequence 3, Appl
7	180.6	49.5	597	1 US-08-968-505-3	Sequence 3, Appl
8	180.2	49.4	561	1 US-08-905-314A-24	Sequence 24, Appl
9	174.4	47.8	590	4 US-09-026-601-41	Sequence 41, Appl
10	171.8	47.1	531	1 US-08-652-127C-8	Sequence 7, Appl
11	171	46.8	583	1 US-08-652-127C-8	Sequence 8, Appl
12	170.8	46.8	581	4 US-08-652-127C-6	Sequence 6, Appl
13	170.4	46.7	579	4 US-09-026-601-38	Sequence 38, Appl
14	169.6	46.5	580	4 US-09-026-601-37	Sequence 37, Appl
15	169.2	46.4	579	4 US-09-026-601-29	Sequence 29, Appl
16	169.2	46.4	579	4 US-09-026-601-30	Sequence 30, Appl
17	169.2	46.4	579	4 US-09-026-601-34	Sequence 34, Appl
18	169.2	46.4	579	4 US-09-026-601-36	Sequence 36, Appl
19	168.8	46.2	579	4 US-09-026-601-32	Sequence 32, Appl
20	168.8	46.2	580	4 US-09-026-601-40	Sequence 40, Appl
21	168	46.0	545	2 US-08-722-187-85	Sequence 85, Appl
22	167.6	45.9	545	5 PCT-US95-04712-85	Sequence 85, Appl
23	167.6	45.9	545	5 PCT-US95-04712-85	Sequence 85, Appl
24	167.2	45.8	579	4 US-09-026-601-31	Sequence 31, Appl
25	166.8	45.7	588	1 US-08-742-023-5	Sequence 5, Appl
26	166.8	45.7	588	3 US-08-968-505-5	Sequence 5, Appl
27	166.6	45.6	580	4 US-09-026-601-33	Sequence 33, Appl

28	166.4	45.6	588	1 US-08-742-023-4	Sequence 4, Appl
29	166.4	45.6	588	3 US-08-968-505-4	Sequence 4, Appl
30	166.4	45.6	594	1 US-08-652-127C-5	Sequence 5, Appl
31	165.8	45.4	548	1 US-08-233-608-1	Sequence 1, Appl
32	165.8	45.4	548	1 US-08-887-480-1	Sequence 1, Appl
33	165.8	45.4	548	2 US-08-722-187-1	Sequence 1, Appl
34	165.8	45.4	548	5 PCT-US95-04712-1	Sequence 1, Appl
35	165.6	45.4	556	1 US-08-887-480-85	Sequence 85, Appl
36	165.6	45.4	556	1 US-08-905-314A-23	Sequence 23, Appl
37	165.4	45.3	626	1 US-08-233-608-3	Sequence 3, Appl
38	165.4	45.3	626	1 US-08-887-480-3	Sequence 3, Appl
39	165.4	45.3	626	2 US-08-722-187-3	Sequence 3, Appl
40	165.4	45.3	626	4 US-09-635-747-38	Sequence 38, Appl
41	165.4	45.3	626	5 PCT-US95-04712-3	Sequence 3, Appl
42	165	45.2	546	1 US-08-887-480-96	Sequence 96, Appl
43	165	45.2	546	1 US-08-905-314A-22	Sequence 22, Appl
44	165	45.2	605	3 US-08-968-727-1	Sequence 1, Appl
45	163.8	44.9	534	1 US-08-233-608-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-037-9908-7
; Sequence 7, Application US/090379908
; Patent No. 6248519
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; DESCENZO, Richard A.
; MORENZONI, Richard A.
; IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,9908
; FILING DATE: 11-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 29520/30001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-037-9908-7

Query Match 70.1%; Score 256; DB 4; Length 556;
 Best Local Similarity 88.5%; Pred. No. 4.3e-68;
 Matches 324; Conservative 0; Mismatches 35; Indels 7; Gaps 4;

OY 1 aaattcaacaatgagctcttgggttcgagcgtatgaagaacgacgaactcgat 60
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 Db 175 AAACCTTCAACACGAGTCTTGGTTCGGCATCGATGAAGAACCCAGCAATGCGAT 224
 OY 61 aagtaatgtaattgcaaatcagtaacatcagatctttaaagcagcatggcccc 120
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 Db 235 ACCTAATGTAATTGCA-AATTCAGTGAATCATCGAGTCTTTAAAGCACATGCGCCCC 293
 OY 121 ctggcattccgggggagcagctctgcagagcgtcattgctgcctcaagccgagctgtg 180
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 Db 294 CTGATATTCGGGGGGGCGATCCGTCCGACGCTATTGCTGCCCTCAAGCCGGCTTGG 353
 OY 181 ttatggatctgctccccccccccgggggagcggccgaaagcagcggcgacgg -gt 239
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 Db 354 TGTGGGCCCCCTCTCCCAATTCGGGGGACGGGCCGAAAGCACGGCGCGCGCT 413
 OY 240 ccggtccctcagcgtatg99gcttgctcaaccgctcgtatgaaggcggcgccgacg 299
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 Db 414 CCGGTCTCGACGGTATGGGGCTTTGTCAACCCCTC--TGTAGCCCCGGCGCGCTTGC 471
 OY 300 cggcgctcccaacctatcttctcaggttgacctgagtcagtgataggaataccgctga 359
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 Db 472 CGATCAACCCCAATTT--TTATCCAGGTTGACCTCGGATGAGTGGGATACCGCTGA 528
 OY 360 actaa 365
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 Db 529 ACTTAA 534

RESULT 2

US-09-037-990B-6
 : Sequence 6, Application US/09037990B
 : Patent No. 6248519

GENERAL INFORMATION:

APPLICANT: ENGEL, Stacia R.

DESCENZO, Richard A.

MORENZONI, Richard A.

IRELAN, Nancy A.

TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/037, 990B

FILING DATE: 11-Mar-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Jeffrey S.

REGISTRATION NUMBER: 31,879

REFERENCE/DOCKET NUMBER: 29520/30001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 498 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-037-990B-6

Query Match 60.4%; Score 220.6; DB 4; Length 498;
 Best Local Similarity 90.8%; Pred. No. 1.9e-57;
 Matches 268; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

OY 1 aaattcaacaatgagctcttgggttcgagcgtatgaagaacgacgaactcgat 60
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 Db 176 AAACCTTCAACACGAGTCTTGGTTCGGCATCGATGAAGAACCCAGCAATGCGAT 235
 OY 61 aagtaatgtaattgcaaatcagtaacatcagatctttaaagcagcatggcccc 120
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 Db 236 ACCTAATGTAATTGCA-AATTCAGTGAATCATCGAGTCTTTAAAGCACATGCGCCCC 294
 OY 121 ctggcattccgggggagcagctctgcagagcgtcattgctgcctcaagccgagctgtg 180
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 Db 295 CTGATATTCGGGGGGGCGATCCGTCCGACGCTATTGCTGCCCTCAAGCCGGCTTGG 354
 OY 181 ttatggatctgctccccccccccgggggagcggccgaaagcagcggcgacgg -g 238
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 Db 355 TGTGGGCCCCCTCTCCCAATTCGGGGGACGGGCCGAAAGCACGGCGCGCGCT 414
 OY 239 tccggtccctcagcgtatg99gcttgctcaaccgctcgtatgaaggcggcgacg 293
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 Db 415 TCCGTCTCGACGGTATGGGGCTTTGTCAACCCCTCTGTAGGCCCGCGCGCGC 469

RESULT 3

US-08-986-727-4

: Sequence 4, Application US/08986727

: Patent No. 6080543

GENERAL INFORMATION:

APPLICANT: ENGEL, Stacia R.

DESCENZO, Richard A.

MORENZONI, Richard A.

IRELAN, Nancy A.

TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/986,727

FILING DATE: 08-DEC-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ekslorn, Richard C.

REGISTRATION NUMBER: 37,027

REFERENCE/DOCKET NUMBER: 009773-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 611 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-986-727-4

Query Match 56.7%; Score 206.8; DB 3; Length 611;
Best Local Similarity 76.8%; Pred. No. 2,9e-53;
Matches 281; Conservative 0; Mismatches 77; Indels 8; Gaps 2;

OY 1 aaacttcaacaatgagatctcttggttcgagcatcagtaagaacgacgaactgcgat 60
DB 232 AAATTTCACCAACGATCTCTGTGTCGATCATCATGAAGAACGACGAAATCGCAT 291
OY 61 aagtaatgtaattgacgaattcagtgatcatcagctcttgaagacattgacgccc 120
DB 292 AAGTAATGTAATTGCAAGATTGAGTGAATCATGAAATCTTGAACGACCATGCGCCCT 351
OY 121 ctggacatccgggggagcatgctctgcagagcgatcatgtctgacctcaagccggcttg 180
DB 352 CTGGTATTCGAGGAGCATGCTGTTCGAGCGTCATTTTCMAACCTCAAGCCTGGCTTG 411
OY 181 tgttggtcgtgctgccccccccgggggagcgagccgaaagcgacgagcgacgctgc 240
DB 412 GATGGGCACTGCTCCCGCCCGGGGAGCGAGCCCTGAATCACTGAGCAGCTG--- 468
OY 241 cggctcgcagcgatgagggctgtgacccgctcgatcagggccggccgggcccagcc 300
DB 469 ----CCAGGACCCCGAGCGAGTGAATTAACCTCGCTCCGGAGGCCCTGGCGGTGCC 524
OY 301 ggcgcttcaacctatcctt-tctcaggttgacctgagtcagtgaggtataccgctga 359
DB 525 TGCGGTTAAACCCCAACTTGTGAAGTTGACCTCGATCAGTGAATACCCGCTGA 584
OY 360 acttaa 365
DB 585 ACTTAA 590

RESULT 4
US-08-986-727-5
Sequence 5, Application US/08986727

Patent No. 6080543
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.
APPLICANT: DESCENZO, Richard A.
APPLICANT: IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,727
FILING DATE: 08-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ekstrom, Richard C.
REGISTRATION NUMBER: 37,027
REFERENCE/DOCKET NUMBER: 009773-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-986-727-5

Query Match 55.8%; Score 203.8; DB 3; Length 568;
Best Local Similarity 76.4%; Pred. No. 2,2e-52;
Matches 279; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

OY 1 aaacttcaacaatgagatctcttggttcgagcatcagtaagaacgacgaactgcgat 60
DB 191 AAATTTCACCAACGATCTCTGTGTCGATCATCATGAAGAACGACGAAATCGCAT 250
OY 61 aagtaatgtaattgacgaattcagtgatcatcagctcttgaagacattgacgccc 120
DB 251 AAGTAATGTAATTGCAAGATTGAGTGAATCATGAAATCTTGAACGACCATGCGCC 310
OY 121 ctggacatccgggggagcatgctctgcagagcgatcatgtctgacctcaagccggcttg 180
DB 311 TTGATATTCGAGGAGCATGCTGTTCGAGCGTCATTAACACCTCAAGCCTGCTGTTG-- 368
OY 181 tgttggtcgtgctgccccccccgggggagcgagccgaaagcgacgagcgacgctgc 240
DB 369 ----CAATTGGGCACTGCTCTACATGCGAGCGCGCTCGAAGACCTCGCGGTGCTGT 424
OY 241 cggctcgcagcgatgagggctgtgacccgctcgatcagggccggccgggcccagcc 300
DB 425 CAGCCCTCAAGCGTGTGAATGATACACCTCGCTTGAGATGTTGGCGTCCGCCCGGAC 484
OY 301 ggcgcttcaacctatccttctcaggttgacctgagtcagtgaggtataccgctga 360
DB 485 GAACCTCTGAACCTTTCT---CAAGGTTGACCTCGATCAGTGAAGGATACCCGCTGA 541
OY 361 cttaa 365
DB 542 CTTAA 546

RESULT 5
US-08-986-727-3

Sequence 3, Application US/08986727
Patent No. 6080543
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.
APPLICANT: DESCENZO, Richard A.
APPLICANT: IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,727
FILING DATE: 08-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ekstrom, Richard C.
REGISTRATION NUMBER: 37,027
REFERENCE/DOCKET NUMBER: 009773-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620

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NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3', end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..181
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note="5', end of large subunit
OTHER INFORMATION: rRNA gene"

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Query Match	49.4%	Score 180.2;	DB 1;	Length 561;
Best Local Similarity	71.8%;	Pred, No. 2.8e-45;		
Matches 265; Conservative	2;	Mismatches 90;	Indels 12;	Gaps 2

Qy	1	aaacttcaacaatgagatcctcttggtttccggacatgaagaagaacgaggaacttgat	60
Db	181	AAACCTTCAACACGACGATCTCTTGTTCTGGCATGCATAMAAACGACGAAATGGGAT	240
Qy	61	aagtaataatgaaattgcagaaattcagatgaatcatcagatctcttggaaacacattgcgcc	120
Db	241	AAGTAATGGAATTCGAGAAATTCAGTGAATCATCGAATCTTTGAACGACACTTTCGCCCG	300
Qy	121	ctggacatccggggggacatgccttgctccagcgtcatctgctgcctcaagccc---gact	176
Db	301	CTGGATTTCCGCGCGGCGATGCTGTTTCAGCCGCAATTTCAACCCCTCAAGCCCCGGGTTT	360
Qy	177	tgt	236
Db	361	GGGTGTGGGGAGTCGCTCTCTCTTTGGCGGTGCCGCCGCCCAATAATGAGCGGTCTC	420
Qy	237	ggtccgcgtccacgaagcgtatgagggtctgtgtacaccgcgtctagtgagcgcggtcgagcc	296
Db	421	G-----CTGCAACCTCATTGCGTAGCTAACACCTTCGCACTGGAACTGGACCGCGCGC	472
Qy	297	agcgcgagcttccaaactcttcttccagttggaaccccgatcaggtgaagataaacccgc	356
Db	473	GGCAGTGGCGCTAAAAACCCCAACTTTCGAAATGTTTGACCTCGATCATCGTAGGAATATCCCGC	532

RESULT 9
US-09-026-601-41
Sequence 41, Application US/09026601
Patent No. 6358680
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6358680artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 63586800th Carolina
COUNTRY: USA
ZIP: 27709

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1  COMPUTER READABLE FORM:
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3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: PatentIn Release #1.0, Version #1.30
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/026,601
9
10 FILING DATE:
11
12 CLASSIFICATION:
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Melgs, J. Timothy
15 REGISTRATION NUMBER: 38,241
16 REFERENCE/DOCKET NUMBER: CGC 1984
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 919-541-8587
19 TELEFAX: 919-541-8689
20 INFORMATION FOR SEQ ID NO: 41:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 590 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: DNA (genomic)
27 ORIGINAL SOURCE:
28 ORGANISM: Pyrenophora teres
29 INDIVIDUAL ISOLATE: 36570
30 IMMEDIATE SOURCE:
31 CLONE: 10-1
32
33 FEATURE:
34 NAME/KEY: misc_feature
35 LOCATION: 1..30
36 OTHER INFORMATION: /note="3' end of small subunit
37 OTHER INFORMATION: rRNA gene"
38 FEATURE:
39 NAME/KEY: misc_feature
40 LOCATION: 31..209
41 OTHER INFORMATION: /note="ITS1"
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: 210..366
45 OTHER INFORMATION: /note="5.8S rRNA gene"
46 FEATURE:
47 NAME/KEY: misc_feature
48 LOCATION: 367..536
49 OTHER INFORMATION: /note="ITS2"
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: 537..590
53 OTHER INFORMATION: /note="5' end of large subunit
54 OTHER INFORMATION: rRNA gene"
55
56 US-09-026-601-41

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Query Match	47.88;	Score 174.4;	DB 4;	Length 590;
Best Local Similarity	70.98;	Pred. No. 1.6e-43;		
Matches 258; Conservative	1;	Mismatches 102;	Indels 3;	Gaps 2;

Qy	2	aacttcaacaatgagcctccttggtccgggcatcagatgaagaagcagcgaaactgcatgata	61
Db	210	AACTTTCAACCAACGGATCTCTTGTTCTGGCATTCGATGAAGAAACGACGAAATTCGATA	269
Qy	62	agcaatggaattggaagaattcagtgatcatcatcagatgcttttgaagacacattggccccc	121
Db	270	AGTAGTGTAATTTGGAGAAATTCAGTGAAATATCGAAATCTTTGACGCAACATTTGGCCCTT	329
Qy	122	tggcattccggggggagcagtcctgcgcagcagcatctgctcgcctccaagcccgactgtgt	181
Db	330	TGGTATTCCAAAGGACATGCTGTTTCAGAGGCTCATTTGTAAACCTCAAGCTTTGGCTG-GT	388
Qy	182	gttggtgtcgtcgtcccccccccgggggagcgggcccgaagaagcagcggcgacagcgtcc	241
Db	389	GTGTGGGCGCTTTTGTCTCTCTCCCGGAGACTCGCTTTAAAAACATTGGCACCGGCTTAC	448

QY 242 ggtcctcagcgtatggtgctgtcaccgcctcgaattagggccggccggccagccg 301
DB 449 TCGTTTCGGAGCCGACACATTTATTTGCGCTTGTTCAGCCCGCGCTCCGCTC--CAT 506
QY 302 ggcctcccaacctatcttctcaggtgacctcgatcaggtaggatatacccgctgaac 361
DB 507 GAAGCCTTTTCTTTTCTTTCAGCCTTTTGACTCTCGGATCAGTAGGAGATACCCGCTGAAC 566
QY 362 ttaa 365
DB 567 TTAA 570

RESULT 10
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-7

Query Match 47.1%; Score 171.8; DB 1; Length 531;
Best Local Similarity 72.4%; Pred. No. 9.4e-43;
Matches 267; Conservative 0; Mismatches 89; Indels 13; Gaps 3;

QY 237 gttccgtctcagagcgtatggtgctgtcaccgcctcgaattagggccggccggccg 296
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QY 297 agccgggtctcccaacctatcttctcaggttgacctcgatcaggtaggatataccgcg 356
DB 444 -CACGCCGTTAAACCCCGCACTTGTGAAGAGTTGACCTCGGATCAGTAGAATAACCCGC 502
QY 357 tgaactaa 365
DB 503 TGAATTAA 511

RESULT 11
US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match 46.8%; Score 171; DB 1; Length 583;
Best Local Similarity 72.5%; Pred. No. 1.7e-42;
Matches 266; Conservative 0; Mismatches 90; Indels 11; Gaps 3;


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Sequence 38, Application US/09026601
Patent No. 6358680
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6358680artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6358680th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026.601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1984
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Pyrenophora tritici-repentis
INDIVIDUAL ISOLATE: 407
IMMEDIATE SOURCE:
CLONE: 7-3-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..208
OTHER INFORMATION: /note= "ITS1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 209..365
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 366..526
OTHER INFORMATION: /note= "ITS2"
FEATURE:
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US-09-026-601-38
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Best Local Similarity 70.9%: Pred. No. 2,6e-42;
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Db 269 AGTAGTGAATATGCGAATTCAGTAATCATCATTTTGAAGCAGCATATGCCCTT 328
Qy 122 tggatccgggggagatccctgctcgaacgcgcatctgctgcacccctaagccgctgtg 181
Db 329 TGGATATTCAGAGGCGATCCTGTTCGACGCGATATTGACCTCAAGCTTTGCTGGTG 388
Qy 182 gtgggtcgtcgtcccccgcgggagcgggcccgaagaagcagcgagcagcgctc 241
Db 389 TTGGGGGTCTGTCTCTCC---GAGACTGCGCTTAATCATTTGGCAGCGGCGTAC 445
Qy 242 ggtcctcgaagcgtatgggcttggtcaccgctcgattagggccggcgccgaagcg 301
Db 446 TGGTTTCGAGCGCACACATATTATTTGCGCTGTTCAGCGCGCTCG-----C 495
Qy 302 ggcgtccaaactatcttcaggttcaggtcagatcagtaagtaagataccgcgtgac 361
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RESULT 15
US-09-026-601-37
Sequence 37, Application US/09026601
Patent No. 6358680
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6358680artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6358680th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026.601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1984
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Pyrenophora tritici-repentis
INDIVIDUAL ISOLATE: 109
IMMEDIATE SOURCE:
CLONE: 6-2
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..209
OTHER INFORMATION: /note= "ITS1"
FEATURE:
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OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 367..527
OTHER INFORMATION: /note= "ITS2"
FEATURE:
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LOCATION: 528..580
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-09-026-601-37
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Best Local Similarity 70.3%; Pred. No. 4.5e-42;
Matches 256; Conservative 3; Mismatches 92; Indels 13; Gaps 2;
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QY 62 agtaatggaatgagaaatcagaaatcagaaatcagaaatcagaaatcagaaat 121
DB 270 ACTAGTGAATGCAAGATTCAGTAATCAATCTTGAACGACATTCGCCCTT 329
QY 122 tggcatccgggggagcagcagcagcagcagcagcagcagcagcagcagcagc 181
DB 330 TGGTATTCGAAGGCGATGCGTTCGAGCGCATTTGACCTCAACCTTGGCTG 389
QY 182 gtcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 241
DB 390 TTGGCTGCTTGTCTCTCC--GAGACTCGCCTTAATAATCATTTGGACGCGCTAC 446
QY 242 gtcctcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 301
DB 447 TGGTTCCGAGCGCAGCACATTTATTTGCGCTTGTTCACCGCGGTG-----C 496
QY 302 gcgtcccaaccttacttctcaggttgacccgacatcaggttaggaataccgctgaac 361
DB 497 GCGTCATGAACCTTCTTCAACCTTTTGACCTCGATCAGTAGATACCGCGTGAAC 556
QY 362 ttaa 365
DB 557 TMAA 560
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Search completed: August 21, 2002, 22:12:23
Job time: 3696 sec

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:01:55 ; Search time 8184.59 Seconds

(without alignments)
964.830 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-10-046-955-5
365
1 aaacttcacacatgatctc.....gggataccgcgtgaacttaa 365

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_MA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365	100.0	365	18 US-09-423-233-5	Sequence 5, Appl1
2	334.8	91.7	565	22 US-09-580-797-36	Sequence 36, Appl1
3	334.8	91.7	9143	18 US-09-404-520-5563	Sequence 5963, Ap
4	333.2	91.3	438	52 US-60-132-861-8175	Sequence 8175, Ap
5	333.2	91.3	568	52 US-60-132-861-7761	Sequence 7761, Ap
6	332.2	91.0	574	52 US-60-132-861-10156	Sequence 10156, A
7	321.8	88.2	642	22 US-09-580-797-6	Sequence 6, Appl1
8	316	86.6	381	52 US-60-132-861-7287	Sequence 7287, Ap
9	308.2	84.4	551	52 US-60-132-861-9331	Sequence 9331, Ap
10	306.4	83.9	559	22 US-09-580-797-39	Sequence 39, Appl1
11	299.8	82.1	552	18 US-09-404-520-17184	Sequence 17184, A
12	293.4	80.4	646	22 US-09-580-797-3	Sequence 3, Appl1
13	284.2	77.9	365	18 US-09-423-233-3	Sequence 11599, A
14	279.8	76.7	7997	47 US-60-082-300-11599	Sequence 3, Appl1
15	278.2	76.2	597	22 US-09-580-797-35	Sequence 35, Appl1
16	273.8	75.0	359	22 US-09-580-797-37	Sequence 37, Appl1
17	273	74.8	601	52 US-60-132-861-6688	Sequence 6688, Ap
18	272.6	74.7	700	22 US-09-580-797-30	Sequence 30, Appl1
19	272	74.5	608	22 US-09-580-797-38	Sequence 38, Appl1
20	265.2	72.7	674	22 US-09-580-797-7	Sequence 7, Appl1
21	260.8	71.5	676	22 US-09-580-797-5	Sequence 5, Appl1
22	259	70.9	685	22 US-09-580-797-4	Sequence 4, Appl1
23	258.8	70.9	344	18 US-09-423-233-2	Sequence 2, Appl1
24	256	70.1	556	1 PCT-US99-04251-7	Sequence 7, Appl1
25	256	70.1	556	14 US-09-037-990-7	Sequence 34, Appl1
26	252.8	69.3	595	22 US-09-580-797-34	Sequence 20902, A
27	239.8	65.7	576	18 US-09-417-507-29902	Sequence 8, Appl1
28	239.8	65.7	672	22 US-09-580-797-8	Sequence 4, Appl1
29	230.4	63.1	355	18 US-09-423-233-4	Sequence 17173, A
30	230	63.0	850	18 US-09-404-520-17173	Sequence 2, Appl1
31	221.2	60.6	382	16 US-09-241-427-2	

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32 220.6 60.4 498 1 PCT-US99-04251-6 Sequence 6, Appl1
33 220.6 60.4 498 14 US-09-037-990-6 Sequence 6, Appl1
34 219.2 60.1 414 52 US-60-132-861-11629 Sequence 11629, A
35 212.8 58.3 654 22 US-09-580-797-26 Sequence 26, Appl
36 212.8 58.3 700 22 US-09-580-797-16 Sequence 16, Appl
37 210 57.5 692 22 US-09-580-797-17 Sequence 17, Appl
38 206.8 56.7 611 1 PCT-US98-25210-4 Sequence 4, Appl1
39 206.6 55.6 309 18 US-09-423-233-28 Sequence 28, Appl
40 203.8 55.8 568 1 PCT-US98-25210-5 Sequence 5, Appl1
41 201.8 55.3 451 52 US-60-132-861-4200 Sequence 4200, Ap
42 196.4 53.8 465 52 US-60-132-861-6561 Sequence 6561, Ap
43 190.8 52.3 714 22 US-09-580-797-31 Sequence 31, Appl
44 190 52.1 419 52 US-60-132-861-8072 Sequence 8072, Ap
45 188.4 51.6 608 1 PCT-US98-25210-3 Sequence 3, Appl1
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ALIGNMENTS

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RESULT 1
US-09-423-233-5
: Sequence 5, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: 03063-0341MP
: CURRENT APPLICATION NUMBER: US/09/423,233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
US-09-423-233-5
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Best Local Similarity 100.0%; Pred. No. 1,1e-84;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 aaacttcaacaatgatactcttgggtccgcatcgaatgaagaagcagcgcaactgcgat 60
OY 61 aagtaatgtaattgcagaatcagtaatacgcagcttgaacgacattgcgccc 120
DB 61 aagtaatgtaattgcagaatcagtaatacgcagcttgaacgacattgcgccc 120
OY 121 ctggcaatccgggggagatgcctgtccagcgatcgtcgtccctcaagcccgctgtg 180
DB 121 ctggcaatccgggggagatgcctgtccagcgatcgtcgtccctcaagcccgctgtg 180
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DB 361 cttaa 365
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RESULT 2
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: Sequence 36, Application US/09580797
: GENERAL INFORMATION:
: APPLICANT: Iwen, Peter C.
: APPLICANT: Hinrichs, Steven H.
: APPLICANT: Henry, Travis
: APPLICANT: Board of Regents of the University of Nebraska
: TITLE OF INVENTION: Materials and Methods for Molecular
: FILE REFERENCE: UNMC 63149
: CURRENT APPLICATION NUMBER: US/09/580,797
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 36
: LENGTH: 565
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
US-09-580-797-36
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Best Local Similarity 98.4%; Pred. No. 8.4e-77;
Matches 360; Conservative 0; Mismatches 2; Indels 4; Gaps 2;
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DB 243 aagtaatgtaattgcagaatcagtaatacgcagcttgaacgacattgcgccc 302
OY 121 ctggcaatccgggggagatgcctgtccagcgatcgtcgtccctcaagcccgctgtg 180
DB 303 ctggcaatccgggggagatgcctgtccagcgatcgtcgtccctcaagcccgctgtg 362
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DB 363 tgttgggtcgtctgtcccccgcggggagcggccgaaagcgcgcgacacg-gt 419
OY 240 cggctccagcgatctggggtctgtccaccgctcgaatgaaggccggcgcgccacg 299
DB 420 cggctccagcgatctggggtctgtccaccgctcgaatgaaggccggcgcgccacg 479
OY 300 cgggtctcaaccttcttctcaggttgcacctgcagtaacgtagggatacccgctga 359
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OY 360 actaa 365
DB 540 actaa 545
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RESULT 3
US-09-404-520-5963
: Sequence 5963, Application US/09404520
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Ghodssi, Azita
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Timberlake, William E.
: APPLICANT: Yu, Jaehyuk
: TITLE OF INVENTION: Emucella nidulans Genome Sequence and Uses Thereof
: FILE REFERENCE: 38-10(15498)A
: CURRENT APPLICATION NUMBER: US/09/404,520
: CURRENT FILING DATE: 1999-09-23
: NUMBER OF SEQ ID NOS: 44345
: SEQ ID NO 5963
: LENGTH: 9143
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
US-09-404-520-5963
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Query Match 91.7%; Score 334.8; DB 18; Length 9143;
Best Local Similarity 98.4%; Pred. No. 1.3e-76;
Matches 360; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgatactctctgttccgcgcatcgtatgaagaacgacgaaactgcgat 60
|||||
DB 4288 aaacttcaacaatgatactctctgttccgcgcatcgtatgaagaacgacgaaactgcgat 4347
OY 61 aagtaatgtaattgcagaattcaagtaatacatcgagctcttgaacgacatctgcgcc 120
|||||
DB 4348 aagtaatgtaattgcagaattcaagtaatacatcgagctcttgaacgacatctgcgcc 4407
OY 121 ctggcatccgggggcatccctgcgcgaagcgtcatctgtccctcaaaagccgcgtctgt 180
|||||
DB 4408 ctggcatccgggggcatccctgcgcgaagcgtcatctgtccctcaaaagccgcgtctgt 4467
OY 181 tcttggtcgtcgtcccccgcggggggaacggccgaagacgagcgagccg-qt 239
|||||
DB 4468 tcttggtcgtcgtcccccgcggggggaacggccgaagacgagcgagccg-qt 4524
OY 240 ccggtcctcgaagcgtatggggttgaaccgcctcgtatgaagccgagccggcgccagc 299
|||||
DB 4525 ccggtcctcgaagcgtatggggttgaaccgcctcgtatgaagccgagccggcgccagc 4584
OY 300 ccggtcctcgaagcgtatctctcgaagctgaagcgtgaagcgtgaagcgtga 359
|||||
DB 4585 ccggtcctcgaagcgtatctctcgaagctgaagcgtgaagcgtgaagcgtga 4644
OY 360 acttaa 365
|||||
DB 4645 acttaa 4650

RESULT 4
US-60-132-861-8175/c
; Sequence 8175, Application US/60132861
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Timberlake, William E.
; TITLE OF INVENTION: ASPERGILLUS NIDULANS GENOME SEQUENCE AND USES THEREOF
; FILE REFERENCE: 38-21(15485)C
; CURRENT APPLICATION NUMBER: US/60/132,861
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13800
; SEQ ID NO 8175
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-132-861-8175

Query Match 91.3%; Score 333.2; DB 52; Length 458;
Best Local Similarity 98.1%; Pred. No. 2.1e-76;
Matches 359; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgatactctctgttccgcgcatcgtatgaagaacgacgaaactgcgat 60
|||||
DB 404 AAACCTTTCAACATGATCTCTTGTTCCGCGATCGATGAAGAAGCGAAGCGAATGCGAT 345
OY 61 aagtaatgtaattgcagaattcaagtaatacatcgagctcttgaacgacatctgcgcc 120
|||||
DB 344 AAGTAATGTAATTGCAGAAATTCAGTAATCATGAGTCTTTGAACGCAATTCGCGCC 285
OY 121 ctggcatccgggggcatccctgcgcgaagcgtcatctgtccctcaaaagccgcgtctgt 180
|||||
DB 284 CTGGCATTCGGGGGCGGATGCTGTCCGAGCTCATTTGCTGCCCTCAAGCCGGCTTTGTG 225
OY 181 tcttggtcgtcgtcccccgcggggggaacggccgaagacgagcgagccg-qt 239
|||||
DB 224 TCTTGGTGTCTGTCT---CCCGCCCGGGGAGCGCGCGAAAGCAGCGGCGACCGTGT 168

OY 240 ccggtcctcgaagcgtatggggttgaaccgcctcgtatgaagaacgacgagccgagccagc 299
|||||
DB 167 CCGGTCTCTGACCGATGCGGCTTTGTCAACCGCTCGATTAGGGCCGCGCGCCAGC 108
OY 300 ccggtcctcgaagcgtatctctcgaagctgaagcgtgaagcgtgaagcgtga 359
|||||
DB 107 CCGGTCTCTGACCGATGCGGCTTTGTCAACCGCTCGATTAGGGATACCGCTGGA 48
OY 360 acttaa 365
|||||
DB 47 ACTTAA 42

RESULT 5
US-60-132-861-7761
; Sequence 7761, Application US/60132861
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Timberlake, William E.
; TITLE OF INVENTION: ASPERGILLUS NIDULANS GENOME SEQUENCE AND USES THEREOF
; FILE REFERENCE: 38-21(15485)C
; CURRENT APPLICATION NUMBER: US/60/132,861
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13800
; SEQ ID NO 7761
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-132-861-7761

Query Match 91.3%; Score 333.2; DB 52; Length 568;
Best Local Similarity 98.1%; Pred. No. 2.2e-76;
Matches 359; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgatactctctgttccgcgcatcgtatgaagaacgacgaaactgcgat 60
|||||
DB 174 aaacttcaacaatgatactctctgttccgcgcatcgtatgaagaacgacgaaactgcgat 233
OY 61 aagtaatgtaattgcagaattcaagtaatacatcgagctcttgaacgacatctgcgcc 120
|||||
DB 224 aagtaatgtaattgcagaattcaagtaatacatcgagctcttgaacgacatctgcgcc 293
OY 121 ctggcatccgggggcatccctgcgcgaagcgtcatctgtccctcaaaagccgcgtctgt 180
|||||
DB 294 ctggcatccgggggcatccctgcgcgaagcgtcatctgtccctcaaaagccgcgtctgt 353
OY 181 tcttggtcgtcgtcccccgcggggggaacggccgaagacgagcgagccg-qt 239
|||||
DB 354 tcttggtcgtcgtcccccgcggggggaacggccgaagacgagcgagccg-qt 410
OY 240 ccggtcctcgaagcgtatggggttgaaccgcctcgtatgaagccgagccggcgccagc 299
|||||
DB 411 ccggtcctcgaagcgtatggggttgaaccgcctcgtatgaagccgagccggcgccagc 470
OY 300 ccggtcctcgaagcgtatctctcgaagctgaagcgtgaagcgtgaagcgtga 359
|||||
DB 471 ccggtcctcgaagcgtatctctcgaagctgaagcgtgaagcgtgaagcgtga 530
OY 360 acttaa 365
|||||
DB 531 acttaa 536

RESULT 6
US-60-132-861-10156
; Sequence 10156, Application US/60132861
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Timberlake, William E.
; TITLE OF INVENTION: ASPERGILLUS NIDULANS GENOME SEQUENCE AND USES THEREOF
; FILE REFERENCE: 38-21(15485)C
; CURRENT APPLICATION NUMBER: US/60/132,861

RESULT 12
US-09-580-797-3
; Sequence 3, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; APPLICANT: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: Detection of Clinically Relevant Pathogenic Fungal Species
; CURRENT APPLICATION NUMBER: US/09/580.797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Aspergillus ustus
US-09-580-797-3

Query Match 80.4%; Score 293.4; DB 22; Length 646;
Best Local Similarity 96.6%; Pred. No. 5.1e-66;
Matches 343; Conservative 0; Mismatches 6; Indels 6; Gaps 4;

QY 1 aaattcaacaatgagctcttggctccgagcatgaaagaacgcagcaactgcgat 60
|||||
DB 295 aaacttcaacaatgagctcttggctccgagcatgaaagaacgcagcaactgcgat 354
61 aagtaatggaatgcaaatcagtaacatcgaagctcttgaacgacacttgccccc 120
|||||
DB 355 aagtaatggaatgcaaatcagtaacatcgaagctcttgaacgacacttgccccc 414
121 ctggcaatccgggggagcatgctctgcagagcgtacatgtctgccc-tcaagccggctgt 179
|||||
DB 415 ctggcaatccgggggagcatgctctgcagagcgtacatgtctgccc-tcaagccggctgt 474
180 gttgtgggtcgtcgtcccccgggggagagccggaagcagcgccgacccg-g 238
|||||
DB 475 gttgtgggtcgtcgtcccccgggggagagccggaagcagcgccgacccg-g 531
239 tccggtccctcgaagcgtatagggcgttcgaacccgctgattagggccggcgcccgca 298
|||||
DB 532 tccggtccctcgaagcgtatagggcgttcgaacccgctgattagggccggcgcccgca 591
QY 299 ccggcgctcccaacctat-cttctcaggttgacctcgagatcaggttagggatac 352
|||||
DB 592 ccggcgctcccaacctat-cttctcaggttgacctcgagatcaggttagggatac 646

RESULT 13
US-09-423-233-3
; Sequence 3, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: Other Filamentous Fungi
; CURRENT APPLICATION NUMBER: US/09/423.233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-09-423-233-3

Query Match 77.9%; Score 284.2; DB 18; Length 365;
Best Local Similarity 91.3%; Pred. No. 1.2e-63;

Matches 335; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

QY 1 aaattcaacaatgagctcttggctccgagcatgaaagaacgcagcaactgcgat 60
|||||
DB 1 aaacttcaacaatgagctcttggctccgagcatgaaagaacgcagcaactgcgat 60
61 aagtaatggaatgcaaatcagtaacatcgaagctcttgaacgacacttgccccc 120
|||||
DB 61 aagtaatggaatgcaaatcagtaacatcgaagctcttgaacgacacttgccccc 120
121 ctggcaatccgggggagcatgctctgcagagcgtacatgtctgccc-tcaagccggctgt 180
|||||
DB 121 ctggcaatccgggggagcatgctctgcagagcgtacatgtctgccc-tcaagccggctgt 180
181 ttttgggtcgtcgtccccc-gcccccgggggagagcccggaagcagcgccgacccg-g 238
|||||
DB 181 ttttgggtcgtcgtccccc-gcccccgggggagagcccggaagcagcgccgacccg-g 240
239 tccggtccctcgaagcgtatagggcgttcgaacccgctgattagggccggcgcccgca 298
|||||
DB 241 tccggtccctcgaagcgtatagggcgttcgaacccgctgattagggccggcgcccgca 298
QY 299 ccggcgctcccaacctat-cttctcaggttgacctcgagatcaggttagggatac 358
|||||
DB 299 ccggcgctcccaacctat-cttctcaggttgacctcgagatcaggttagggatac 358
QY 359 aacttaa 365
|||||
DB 359 aacttaa 365

RESULT 14
US-60-082-300-11599
; Sequence 11599, Application US/60082300
; GENERAL INFORMATION:
; APPLICANT: LAGACE, ROBERT E.
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: RUSSO, FRANK D.
; APPLICANT: HANN, AMY L.
; APPLICANT: HEATH, JOE D.
; APPLICANT: FINNEY, GREGORY L.
; APPLICANT: BROOKS, JACQUELINE
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ASPERGILLUS FUMIGATUS
; NUMBER OF SEQUENCES: 21910
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION TRA: A:
; APPLICATION NUMBER: US/60/082,300
; FILING DATE: HERewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-00014 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 11599:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: AFU1C11615
US-60-082-300-11599

Query Match 76.7%: Score 279.8; DB 47; Length 7997;
Best Local Similarity 92.1%: Pred. No. 2,7e-62;
Matches 339; Conservative 0; Mismatches 22; Indels 6; Gaps 4;

OY 1 aaacttcaacatggaatctcttggtccggatcgatgaagaacgacgaactgcgat 60
DB 3993 AAACCTTCAACACGCGATCTTGTTCCGGCATCGATGAAAGCAGCGCAATGCCAT 3992
OY 61 aagtaatgtaattgcagaattcagtaatcagagtccttgaacgacaatgcgccc 120
DB 3993 AAGTAATGTGAATTCGAATAATTCAGTGAATCATGAGACTTTGAACGACATTCGCGCCC 4052
OY 121 ctggatccgggggggagctgctgcgaagcgtatgctccctcaagcccggtctgtg 180
DB 4053 CTGGATTCGGGGGGGAGCTGCTGCAGCGTCAATGCTCCTCAAGCAGCGCTGTG 4112
OY 181 tcttgatcgtcgtccccc-cccccgggggagcgcccgaaagcaagcgcgacgg-9 238
DB 4113 TGTTGGGCCCCCGTCCCTCTCCCGGGGAGCGGCCGGAAGCAGCGCGCACCGCG 4172
OY 239 tccggtcccgagcgtatggtgctgtacccgcgtcatgaagccggcgcgccag 298
DB 4173 TCCGCTCCTCGAGCGTATGGGGCTTTGTCACCTGCTC--TGTAGCCCGCGCGCGCAG 4230
OY 299 ccgggtccccaactcttcttcagaagtacgtcagtagagtagatccgctg 358
DB 4231 CCGAC--ACCCAACTTATTTTCTTAAGTTGACCTCGATCAGTAGAGATACCGCTG 4288
OY 359 aacttaa 365
DB 4289 AACTTAA 4295

RESULT 15
US-09-580-797-35
Sequence 35, Application US/09580797
GENERAL INFORMATION:
APPLICANT: Iwen, Peter C.
APPLICANT: Hinrichs, Steven H.
APPLICANT: Henry, Travis
TITLE OF INVENTION: Board of Regents of the University of Nebraska
TITLE OF INVENTION: Materials and Methods for Molecular
FILE REFERENCE: UNKC 63149
CURRENT APPLICATION NUMBER: US/09/580,797
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 597
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-09-580-797-35

Query Match 76.2%: Score 278.2; DB 22; Length 597;
Best Local Similarity 92.1%: Pred. No. 4.6e-62;
Matches 338; Conservative 0; Mismatches 23; Indels 6; Gaps 4;

OY 1 aaacttcaacatggaatctcttggtccggatcgatgaagaacgacgaactgcgat 60
DB 215 aaacttcaacacgagctccttggtccggatcgatgaagaacgacgaactgcgat 274
OY 61 aagtaatgtaattgcagaattcagtaatcagagtccttgaacgacaatgcgccc 120
DB 275 aactaatgtaattgcagaattcagtaatcagagtccttgaacgacaatgcgccc 334

OY 121 ctggatccgggggggagctgctgcgaagcgtatgctccctcaagcccggtctgtg 180
DB 335 ctggtatccgggggggagctgctgcgaagcgtatgctccctcaagcagcggtctgtg 394
OY 181 tcttgatcgtcgtccccc-cccccgggggagcgcccgaaagcaagcgcgacgg-9 238
DB 395 tcttggtcccggtcccccctcccggggagcgcccgaaagcaagcgcgacggcgcg 454
OY 239 tccggtcccgagatggtgctgtgtacccgcgtcatgaagcgcgccggcgcgacg 298
DB 455 tccggtcccgagatggtgctgtgtacccgcgtcatgaagcgcgccggcgcgacg 512
OY 299 ccgggtccccaactcttcttcagaagtacgtcagtagagtagatccgctg 358
DB 513 ccgac--accacaacttatttcttaagtgaccccgatcagtagagtagatcccgctg 570
OY 359 aacttaa 365
DB 571 aacttaa 577

Search completed: August 22, 2002, 00:39:26
Job time: 13051 sec

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[illegible]

```

: RESULT 2
: US-10-046-955-3
: Sequence 3, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Etrol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus niger
: US-10-046-955-3

```

Query Match	77.9%	Score 284.2	DB 7	Length 365
Best Local Similarity	91.3%	Pred. No. 3,4e-68		
Matches 333	Conservative 0	Mismatches 28	Indels 4	Gaps 3
OY	1	aaacttcacaacatgagatcctctgtgtccgagatcatgtaagaacgcagcaactcgat	60	
Db	1	aaacttcacaacatgagatcctctgtgtccgagatcatgtaagaacgcagcaactcgat	60	
OY	61	aagcaatgtgaattgcagaatccagtgaatcatcgaagctctttgaacgcacattgcgccc	120	
Db	61	aaccaaatgtgaattgcagaatccagtgaatcatcgaagctctttgaacgcacattgcgccc	120	
OY	121	ctgggcatcccgggggcagctgcgtccgcagcgctaatgtcgccctcaagccggctgtg	180	
Db	121	ctggatctccgggggcagctgcgtccgcagcgctaatgtcgccctcaagcagggctgtg	180	
OY	181	tgtttgggtgcgtgcgtccccc-cccccggggagcggcccgaaagtcagtcgggacacg-9	238	
Db	181	tgtttgggtgcgtgcgtcccccctccgggggagcggcccgaaagtcagtcgggacacg-9	240	
OY	239	tccggctccctcagcagatgaggtgtgtgcacacccctcgattgaaggccggccggcgccag	298	
Db	241	tccgactccctcagcagatgaggt	298	
OY	299	ccggcgctcccaacttatcttcttcaggtttgacatcgcagatcagatagataccgctg	358	

Db 299 CGCAGCTTATCCACCACTTTTTCAGGTGACCTGGATCAGTLAGGATACCCGCTG 358
QY 359 AACCTAA 365
Db 359 AACCTAA 365

```

1      RESULT      3
2      US-10-046-955-2
3      ; Sequence 2, Application US/10046955
4      ; GENERAL INFORMATION:
5      ; APPLICANT: The Government of the United States of America, as Represented by the
6      ; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
7      ; APPLICANT: Control and Prevention
8      ; APPLICANT: Morrison, Christine J.
9      ; APPLICANT: Reiss, Errol
10     ; APPLICANT: Aldorevich, Lilliana
11     ; APPLICANT: Choi, Jong Soo
12     ; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
13     ; TITLE OF INVENTION: Other Filamentous Fungi
14     ; FILE REFERENCE: 6395-62064
15     ; CURRENT APPLICATION NUMBER: US/10/046,955
16     ; CURRENT FILING DATE: 2002-06-04
17     ; PRIOR APPLICATION NUMBER: US 09/423,233
18     ; PRIOR FILING DATE: 2000-06-27
19     ; PRIOR APPLICATION NUMBER: PCT/US98/08926
20     ; PRIOR FILING DATE: 1998-05-01
21     ; PRIOR APPLICATION NUMBER: US 60/045,400
22     ; PRIOR FILING DATE: 1997-05-02
23     ; NUMBER OF SEQ ID NOS: 61
24     ; SOFTWARE: PatentIn Ver. 2.0
25     ; SEQ ID NO 2
26     ; LENGTH: 364
27     ; TYPE: DNA
28     ; ORGANISM: Aspergillus fumigatus
29     US-10-046-955-2

```

Query Match	70.98;	Score 258.8;	DB 7;	Length 364;
Best Local Similarity	90.58;	Pred. No. 3e-61;		
Matches 333;	Conservative 0;	Mismatches 27;	Indels 8;	Gaps 5;
QY 1	aaacttcaacaatgagatctctctgtgtccggatcgtatgaaagacgcagcgaaatcgat	60		
Db 1	aaacttcaacaatgagatctctctgtgtccggatcgtatgaaagacgcagcgaaatcgat	60		
QY 61	aagtaatgtgaattgcagaattcaatgtaattcaatcagatgcttttgaacgcacatgtgcgcc	120		
Db 61	aactaaatgtgaattgcagaattcaatgtaattcaatcagatgcttttgaacgcacatgtgcgcc	120		
QY 121	ctggcatctccgggggagatcgcgtccgcggagcgatctgtccccc-tcaacccggcttat	179		
Db 121	ctgttatctccgggggagatcgcgtccgcggagcgatctgtccccc-tcaacaaagcgcttat	180		
QY 180	gtgtgtgtgtcgtcgtccccc-ccccgggggagacgggccgaagacagcgcgacacg-	237		
Db 181	gtgtgtgtgtcgtcgtcccccctccctctccgggggagcgggccgaagacagcgcgacacgcg	240		
QY 238	gtccgggcccgcggagctatgaggcttgttaaccgcgcctcgtatgaggcgcgcgcgca	297		
Db 241	gtccgggcccgcggagctatgaggcttgttcaaccgcgcctcgtatgaggcgcgcgcgca	297		
QY 298	gcgcggctctcaacctatcttcttcagatgttgaccctcgatcaggtatgagataaccgct	357		
Db 298	gcgcgac-acccaacctattttcttaagtgtgaccctcgatcaggtatgagataaccgct	355		
QY 358	gaacttaa 365			
Db 356	gaacttaa 363			

Query Match	63.18;	Score 230.4;	DB 7;	Length 355;
Best Local Similarity	87.68;	Pred. No. 1.7e-53;		
Matches 312; Conservative	0;	Mismatches 31;	Indels 13;	Gaps 5

```

RESULT      5
US-10-046-955--28
: Sequence 28, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for DIS
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955

```

Query Match	56.6%	Score 206.6	DB 7	Length 309
Best Local Similarity	87.0%	Pred. No. 5.4e-47		
Matches 274; Conservative	0	Mismatches 34	Indels 7	Gaps 4

RESULT 6
US-09-766-173C-4
; Sequence 4, Application US/09766173C

```

? APPLICANT: Carroll, George C.
? TITLE OF INVENTION: Materials and Methods For Detection of
? TITLE OF INVENTION: Pathogenic Gulgnardia Citricarpa
? FILE REFERENCE: Oregon 99-09
? CURRENT APPLICATION NUMBER: US/09/766,173C
? PRIOR FILING DATE: 2001-01-22
? PRIOR APPLICATION NUMBER: PCT/US01/01735
? PRIOR FILING DATE: 2001-01-19
? PRIOR APPLICATION NUMBER: 60/177,013
? PRIOR FILING DATE: 2000-01-19
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4
? LENGTH: 641
? TYPE: DNA
? ORGANISM: Gulgnardia Citricarpa
US-09-766-173C-4

```

Query Match	51.9%	Score 189.4;	DB 5;	Length 641;
Best Local Similarity	73.7%;	Pred. No. 3.1e-42;		
Matches 272;	Conservative	0;	Mismatches 86;	Indels 11;
			Gaps	2;

Db	267	aaacttcaaaaacaggaactctcttgctctcgacatcgatgaagacgaaggaatcgat	3256
Oy	61	aagtaaattgaattcgacgaattcagtgaaatccagatctcttgaagacacattcgcccc	120
Db	327	aagtaattgaaattcgacgaattcagtgaaatccagatctcttgaagacacattcgcccc	386
Oy	121	ctggagatctcggggggcgaatgcctctccgagagtgatattgctgcgcccgaagccgggcttg	180
Db	387	ctggagatctcggggggcgaatgcctctccgagagtgatattgctgcgcccgaagccgggcttg	446
Oy	181	tgttggatcgctctgcctcccccgcggggggaaggggcccgaagggcagggctgcgaccgctc	240
Db	447	atgg-----gcagagctcgctgcgagcgccgcgggaagacctgcggcagcgctct	499
Oy	241	cggtctctcgagcgtatgggggcttgtaaccgcgcgaattgaaggccggccggggccag--	298
Db	500	cagctctgagcgtatgtaataataatctgcctcttggaaggaggggggcgcgcggccggga	559
Oy	299	--ccggcgctctccaacctattcttcttcagatttgacactcgatccagtgaaaggaataccgc	356
Db	560	caatcgacctcggtcaactattcttctccaaggttgacctcgatccagtgaaaggaataccgc	619
Oy	357	tgaacttaa	365
Db	620	tgaacttaa	628

RESULT 7
US-09-766-173C-5

```

? Sequence 5, Application US/09/06b1/3C
? GENERAL INFORMATION:
? APPLICANT: Carroll, George C.
? TITLE OF INVENTION: Materials and Methods For Detection of
? TITLE OF INVENTION: Pathogenic Guinardia Citricarpa
? FILE REFERENCE: Oregon 99-09
? CURRENT APPLICATION NUMBER: US/09/766,173C
? PRIOR FILING DATE: 2001-01-22
? PRIOR APPLICATION NUMBER: PCT/US01/01735
? PRIOR FILING DATE: 2001-01-19
? PRIOR APPLICATION NUMBER: 60/177,013
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: fastseq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 618
? TYPE: DNA
? ORGANISM: Guinardia Citricarpa
US-09-766-173C-5

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Query Match	50.4%;	Score 184;	DB 5;	Length 618;
Best Local Similarity	73.1%;	Pred. NO. 9.2e-41;		
Matches 266;	Conservative 0;	Mismatches 90;	Indels 8;	Gaps 2

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Oy 1 aaacttcaacaatggaatcctcttggcttcgcgcgaatcgcgtgaagaacgaagcaatcgcgat 60
Db 262 aaacttcaacaagaaggaatccttggcttcttgcgcgtatggaagcaagcagaatcgcgat 321
Oy 61 aagtaatgtaataatgcagaatctcaatgtaatcaatcgaatcctttgaagcacatctgcgcct 120
Db 322 aagtaatgtaataatgcagaatctcaatgtaatcaatcgaatcctttgaagcacatctgcgcct 381
Oy 121 ctgcgaatctcgggggagcgaatgcctcttcgcgaagcgtatcattgctgcacctcaagccgcgctgtg 180
Db 382 ctggtatctcgggagcgaaatgcctgtctcgaagcgtatcattcaacctcaagctctgtctgtg 441
Oy 181 tgttgggtgcgcgcgcctccccccccccgggggagcgccgaagcgacgagcgagcgacgcgtc 240
Db 442 atctgg-----gcacagctcgcgcgcgcgaagcgagccttgaagccctcgcgcgaacgagcgctcc 494
Oy 241 cgcgtctcgaagcgtatgagcgcttggctacacgcgctcgaattgaaggccgcgcgcgcgcgcagc 299

```

Db 495 tagctctgagcgtagtagtaanaatatctcgcttggagtgctcggtgcgacgcgcgcgcgac 554

QY 300 cggcgctcccaacctatcttctcaggttgaactggatcagtaggataacccgtga 359

Db 555 aatcgaccttcggtctatcttctccaagctgcacctcgatcaggtatggatbaaccctga 614

QY 360 acct 363

Db 615 acct 618

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RESULT      8
PCT-US02-11769-2
; Sequence 2, Application PC/TUS0211769
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; TITLE OF INVENTION: Mankef, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AO 2019_40
; CURRENT APPLICATION NUMBER: PCT/US02/11769
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Muscador albus
PCT-US02-11769-2

```

Query Match	46.3%	Score 169;	DB 1;	Length 652;
Best Local Similarity	70.7%	Pred. No. 1.2e-36;		
Matches 258;	Conservative	0;	Mismatches 95;	Indels 12; Gaps 2

[illegible]

RESULT 9
US-09-517-790-5
; Sequence 5, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: white, Jr., James F


```

: TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Ru
: TITLE OF INVENTION: Diseases in Plants
: FILE REFERENCE: RU-0093
: CURRENT APPLICATION NUMBER: US/09/517,790
: CURRENT FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 60/123,099
: PRIOR FILING DATE: 1999-03-05
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 5
: LENGTH: 536
: TYPE: DNA
: ORGANISM: Ampelomyces humuli
: US-09-517-790-5

```

Query Match	44.58	Score 162.6	DB 5	Length 536
Best Local Similarity	71.58	Pred. No. 6.3e-35		
Matches 261; Conservative	0	Mismatches 89	Indels 15	Gaps 3

```
QY      2 aaattcaacaatgatctcttggttcgcgcatcgataagaacgcgaacgaactcgcata 61
          |||||
Db     170 aaattcaacaacgagatctcttggtttcgcgcatcgataagaacgcgaacgaactcgcata 229
```

DY 62 agtaatctgaattgcagaattccagtgtacatcgcagtccttgaacgcacattgcccc 121
|||||
Dh 230 ataactgaatttcacaattcatgatcatcaatctttgaacgcacattgcccc 289

Oy 122 tggcattccgaggagcatgtcctgtccagcgatcaattgtctgccctcaagccgcgttgtt 181
||| ||||| ||||||| ||||||| ||| ||||| | ||||| |
Db 360 tttatttcacatggaacatgacctatccaacacatttatcacttcaaaccttactta-af 348

OY 182 gctggtcgtcgccccccgcgggagacggcccgaaggcagcgcgaccggtcc 241

242 ggtcctcagcgtatggtgtcaccgcgtcgtattagggcgcgcgcgcga-gcc 300

301 ggcgctcccaacctatcttctcaggtgacctcgatcaggtagggataccgcgtgaa 360

QY 361 ctaa 365
|||||

200 210 220

RESULT 10

```

PCT- 10
PCT-US02-11769-4
: Sequence 4, Application PC/TUS0211769
: GENERAL INFORMATION:
: APPLICANT: Strobel, Gary
: APPLICANT: Manker, Denise
: TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
: TITLE OF INVENTION: USE
: FILE REFERENCE: AQ 2019.40
: CURRENT APPLICATION NUMBER: PCT/US02/11769
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/283,902
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: 60/363,072
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 650
: TYPE: DNA
: ORGANISM: Muscador roseus
PCT-US02-11769-4

```

Query Match	43.6%	Score 159;	DB 1;	Length 650;
Best Local Similarity	69.0%;	Pred. No. 6.3e-34;		
Matches 252; Conservative	0;	Mismatches 100;	Indels 13;	Gaps 2

QY 1 aaacttcaacaatgatctctctgtgtccgcgatcatgaagaacgcagcaactgcgat 60
|||||
Db 278 aaacttcaacaacacgcgatctctctgcgtctcgcgatgaagaacgcagcaaatgcgat 337
|||||

61 aagtaatcgtgaattgcagaatccagtgaaatcatcagagctcttgaagcagcatatgcgcc 120
 |||||
 338 aagtaatcgtgaattgcagaatccagtgaaatcatcagagctcttgaagcagcatatgcgcc 397

[illegible]

181 ttttggtcgttcgtcccccggggagcggcccgaaagcagcggcgacacgctc 240

241 cggctcctcgagcgatattggtggtcgtgtcaccgcgtcgattagggccggccggccgacgcc 300

301 ggagctccaactatcttctcaggttgacctcgatcaggtagggatacccgctgaa 360

DU	305	CTGCGTGAATAAATCCCTCATAATCAAGGTCGACCCCTGAGATCAGAGATAATCCCTCGAA	024
QY	361	CTTAA	365

DB 625 cclaa 629

```
US-09-517-790-1
; sequence 1, Application US/09517790
; GENERAL INFORMATION:
```

```

; TITLE OF INVENTION: use of Phoma glomerata as a Hyperparasite in the Biocon
; TITLE OF INVENTION: Diseases in plants
; FILE REFERENCE: RU-0093

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: CURRENT FILING DATE: 2000-03-02
 : PRIOR APPLICATION NUMBER: US 60/123,099
 : PRIOR FILING DATE: 1999-03-05
 :

```

;      NUMBER OF SEQ ID NOS. 3
;      SOFTWARE: PatentIn version 3.1
;      SEQ ID NO 1
;      LENGTH: 515

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; TYPE: DNA
; ORGANISM: Phomo glomerata
US-09-517-790-1

```

Query Match	42.1%;	Score 153.8;	DB 5;	Length 515;
Best Local Similarity	88.6%;	Pred. No. 1.6e-32;		
Matches 178; Conservative	0;	Mismatches 22;	Indels 1;	Gaps 1

```

Oy      2 aacttcacaacatgatctcttggttccgcatgatgaagaacgcagcaacttcgata 61
          |||||
Db      187 aacttcacaacagcatctcttggttcttgcgcatgatgaagaacgcagcgaatcgcata 246

```

QY 62 agtaatgtgaattcgagaattcagtgaaatcatcgagtccttgaacgcaattgcgcctc 121
|||||
Db 247 agtaatgtgaattcagaattcagtgaaatcatcatcctttgaacgcaattgcgcctc 306

[illegible]

QY 182 gttggtcgtcgtccccc 202
||||||| | ||| | || |

Query Match:	39.28%	Score 143.2	DB 5	Length 516;
Best Local Similarity	78.98%	Pred. No. 1	3e-29;	
Matches 183;	Conservative 0;	Mismatches 48;	Indels 1;	Gaps 1.

Oy	2	aacttcaacatgatactcttggttcgcgcacatgaatgaagaacgcagcaactgcgata	61
db	202	aacttcaacacacagatcctcttggttcgcgcacatgaatgaagaacgcagcaactgcgata	261

```

RESULT 15
US-10-046-955-7
: Sequence 7, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
:

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:44 : Search time 2238.68 Seconds
(Without alignments)
2981.920 Million cell updates/sec

Title: US-10-046-955-6
Perfect score: 319
Sequence: 1 gaaatgcataaataatgt.....ggaataccgcgtaactaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBml:.*
1: gb_da:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_cm:.*
5: gb_ov:.*
6: gb_pac:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_da:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_com:.*
21: em_or:.*
22: em_ov:.*
23: em_dat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*
29: em_vl:.*
30: em_hcg_hum:.*
31: em_hcg_inv:.*
32: em_hcg_other:.*
33: em_hgo_inv:.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
------------	-------	-------	-------	--------	----	----	-------------

1	319	100.0	319	8	AF117921	AF117921 Nectria h
2	308	96.6	509	8	AF165874	AF165874 Nectria h
3	298.6	93.6	550	8	AF178394	AF178394 Nectria h
4	298.6	93.6	550	8	AF178401	AF178401 Nectria h
5	298.6	93.6	569	8	AF129104	AF129104 Nectria h
6	297	92.4	548	8	AF178397	AF178397 Fusarium
7	294.6	90.5	549	8	AF178398	AF178398 Nectria l
8	288.6	90.3	546	8	AF178413	AF178413 Neocosmos
9	288.2	90.3	548	8	AF178402	AF178402 Fusarium
10	287	90.0	547	8	AF178412	AF178412 Neocosmos
11	285.7	89.5	544	8	NEKITS	L36627 Neocosmospo
12	280.2	87.8	550	8	AF178406	AF178406 Fusarium
13	279	87.5	480	8	AF150466	AF150466 Nectria h
14	279	87.5	480	8	AF150467	AF150467 Nectria h
15	279	87.5	480	8	AF440567	AF440567 Nectria h
16	277.2	86.9	550	8	AF178422	AF178422 Fusarium
17	276.2	86.6	552	8	AF178411	AF178411 Nectria h
18	275.6	86.4	550	8	AF178407	AF178407 Fusarium
19	275.6	86.4	550	8	AF178408	AF178408 Fusarium
20	275	86.2	547	8	NECITS	L36619 Nectria hae
21	270.6	84.8	549	8	AF178409	AF178409 Fusarium
22	269.2	84.4	548	8	AF178416	AF178416 Nectria h
23	268	84.0	548	8	AF178395	AF178395 Nectria h
24	268	84.0	548	8	AF178404	AF178404 Fusarium
25	268	84.0	566	8	AF130142	AF130142 Nectria h
26	267.4	83.8	518	8	AF437761	AF437761 Fungal is
27	265.8	83.3	547	8	AF178410	AF178410 Nectria h
28	265	83.1	545	8	NECITS	L36620 Nectria hae
29	265	83.1	552	8	AF178421	AF178421 Nectria h
30	263	82.4	544	8	AF178399	AF178399 Fusarium
31	262.8	82.4	544	8	NECITS	L36616 Nectria hae
32	262.2	82.2	478	8	AF132801	AF132801 Nectria h
33	262.2	82.2	478	8	AF150459	AF150459 Nectria h
34	262.2	82.2	478	8	AF150460	AF150460 Nectria h
35	262.2	82.2	478	8	AF150461	AF150461 Nectria h
36	262.2	82.2	478	8	AF150462	AF150462 Nectria h
37	262.2	82.2	478	8	AF150463	AF150463 Nectria h
38	262.2	82.2	478	8	AF150464	AF150464 Nectria h
39	261.8	82.1	593	8	NH094684	U94684 Nectria hae
40	261.4	81.9	479	8	AF150475	AF150475 Nectria h
41	261.2	81.9	550	8	AF178400	AF178400 Fusarium
42	261.2	81.9	553	8	AF178403	AF178403 Fusarium
43	261.2	81.9	568	8	AF130140	AF130140 Nectria h
44	261.2	81.9	1178	8	FSOITSRGN	L36630 Fusarium so
45	261.2	81.9	1178	8	FSOITSRGN	L36632 Fusarium so

ALIGNMENTS

RESULT 1
AF117921 319 bp DNA linear PLIN 17-JUN-2000
LOCUS Nectria haematococca 5.8S ribosomal RNA gene, partial sequence;
DEFINITION Internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.
ACCESSION AF117921
VERSION AF117921
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 319)
AUTHORS Choi,J.S., Westernman,J.M. and Morrison,C.J.
TITLE Rapid differentiation of filamentous fungi using species-specific
DNA probes
JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE 2 (bases 1 to 319)
AUTHORS Choi,J.S., Westernman,J.M. and Morrison,C.J.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

FEATURES	Location/Qualifiers
source	1..319 /organism="Necteria haematococca" /db_xref="taxon:140110" <1..159 /product="5.8S ribosomal RNA"
rRNA	160..272 /note="ITS2"
misc_RNA	/product="Internal transcribed spacer 2" 273..>319 /product="28S ribosomal RNA"
rRNA	77 a 96 c 84 g 62 t
BASE COUNT	
ORIGIN	

Query Match	100.0%	Score 319:	DB 8:	Length 319:
Best Local Similarity	100.0%	Pred. NO. 1,1e-77:		
Matches 319:	Conservative	0:	Mismatches 0:	Indels 0:
				Gaps 0:
QY	1	gaaatgcgatalaagtaatgtagatccagaattcagtagatcatcgaatccttgaacga	60	
Db	1	GAATAATGGGATATAGTAATCTGAAATTCGCAAAATTCAGTGAATATGAAATCTTTGAACGA	60	
QY	61	catltagccgcgcgcgaattctltagcgagcaatgcctgttcgagcgtcatcaaaccttcag	120	
Db	61	CATTGCGCCCGCCGACGTAATTCGTGGCGGCATGCGCTGTGCAGCGTCATTACAACTCCACG	120	
QY	121	cccccgagccgctgagctltgttgggagtcgaggaagcccccttgagcgacaacgcgcctccca	180	
Db	121	CCCCGGGGCTGTGGCTTTGGGGGATCGCGCGGAACCCCTGTGGCGGCAACAGCGCGTCCCCCA	180	
QY	181	aatacagtgtagcggtccgcgcgcgagcttcatlgtgtatagtaaacactctgcaacttga	240	
Db	181	AATACAGTGGCGGCTGCCCGCCGACGCTTCATTGCTAGTAGTAACCTCCCAACTGGA	240	
QY	241	gagcggtcgagccacagcgcgtlaaaaaaaccaactcttgatgttgcagctcgaatcagtag	300	
Db	241	GAGCGGCGCGGCGACAGCGCTAAACACCCCACTTGTGAATGTTGACCTCGAATCAGTTAG	300	
QY	301	gaataccgcctcgtaactta	319	
Db	301	GAATACCCGCTGAACCTTAA	319	

LOCUS	AP165874	509 bp	DNA	linear	PLN 18-JUL-1999
DEFINITION	Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.				
ACCESSION	AP165874				
VERSION	AP165874.1	GI:5524731			
KEYWORDS					
SOURCE	Nectria haematococca.				
ORGANISM	Nectria haematococca				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.				
AUTHORS	Iwen,P.C., Henry,T. and Hinrichs,S.H.				
TITLE	Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive disease				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 509)				
AUTHORS	Iwen,P.C., Henry,T. and Hinrichs,S.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6495, USA				
FEATURES	Location/Qualifiers				
source	1..509				
	/organism="Nectria haematococca"				
	/strain="ATCC62877"				

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misc_RNA      /db_xref="ATCC:62877"  
               /db_xref="taxon:140110"  
               /note="anamorph: Fusarium solani"  
               1..150  
               /note="ITS1"  
               /product="internal transcribed spacer 1"  
               151..307  
               /product="5.8S ribosomal RNA"  
               308..480  
               /note="ITS2"  
               /product="internal transcribed spacer 2"  
               481..>509  
               /product="28S ribosomal RNA"  
rRNA          130 a 134 c 122 g 103 t  
BASE COUNT  
ORIGIN
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	Query Match	96.6%	Score 308;	DB 8;	Length 509;	
	Best Local Similarity	100.0%	Pred. No. 1,3e-74;			
	Matches 308; Conservative	0;	Mismatches 0;	Indels	0;	Gaps 0;
OY	3 aaatcgaataaaftaatgtgaaattgcagaattacagtaaacatcttgaacgcaca	62				
Db	202 AAATCGAATAATGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	261				
OY	63 ttgcgccgcacgaiaattcttgccgggcacatgcctttcttcgaagcgtaattacaacctcaggcc	122				
Db	262 TTGGCCGCCGCAAGTATCTGGGGGCGCATTGCCGTTCGAGCGTATTACAACTTAGGCC	321				
OY	123 ccgcggccttgacgtttggggatctcgcgcgaagaccctctgcggcacaaacgcgcgtcccca	182				
Db	322 CCGGGCCCTTGCGTGGGGATCGCGGGAGAAGCCCCCTGGGGCACAAACCCGCCCAA	381				
OY	183 tcaactggcagtlcccgcgcagactccaattgcgttgtctaacccttcgaacatggaga	242				
Db	382 TACAATGGCGGTCCCGCCGCAACTTCATTTGGGTATGTAGCTAACCTTCGCAACTGGAGA	441				
OY	243 gcgcgcgcgcacgcgcgttaaacacaccaactlctlaatgttgaacctgcgaatcaagt	302				
Db	442 GCGGCGCGGCACGCGGTAAAAACACCACCAACTTCTGAATGTTGACCTGCAATCAGGTAGA	501				
OY	303 ataaccgc 310					
Db	502 ATACCCGC 509					

LOCUS	AF178394	550 bp	DNA	linear	PLN 20-DEC-2001
DEFINITION	Nectria haematococca mpiv strain NRRL22163 18S ribosomal RNA gene, partial sequence; Internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.				
ACCESSION	AF178394				
VERSION	AF178394.1 GI:10180235				
SOURCE	Nectria haematococca mpiv.				
ORGANISM	Nectria haematococca mpiv.				
REFERENCE	Eukaryote: Fungi: Ascomycota: Pezizomycotina; Sordariomycetes; Hypocreales: Nectriaceae; Nectria.				
AUTHORS	1 (bases 1 to 550)				
TITLE	O'Donnell, K.				
JOURNAL	Molecular phylogeny of the Fusarium solani species complex				
REFERENCE	2 (bases 1 to 550)				
AUTHORS	O'Donnell, K.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA				
FEATURES	Location/Qualifiers				
source	1..550				
	/organism="Nectria haematococca mpiv"				
	/strain="NRRL22163"				

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/note="forma_specialis: xanthoxyli; anamorph: Fusarium
solani f. sp. xanthoxyli"
<1..>550
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"
BASE COUNT      138 a      158 c      137 g      117 t
ORIGIN

Query Match      93.6%; Score 298.6; DB 8; Length 550;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY      3 aaatcgataaagtaatgtgaattgcgaattcgaatcgaatcgaattcgaagcaca 62
        |||||||
DB      235 AAATCGATAAGTAATGTAATGTGAGAAATGCAATCATCGAATCTTTAAACGCACA 294
        |||||||

OY      63 ttggccggccagatatttcggcgaggatcctgttcgagcgtcattacaccccaaggcc 122
        |||||||
DB      295 TTGCGCCGCCAGTATTTGGCGGCGATGCTGTTCGACGTCATTACAACTCTCAGGCC 354
        |||||||

OY      123 cccgggcttggcgttgggagtcgagcagcccccctcgcgagcacaacgcccccaaa 182
        |||||||
DB      355 CCGGGGCTGGCGTTGGGGATCGCGGAGCCGCCCTCGGGGCAC-ACGCCGTCCCTTAA 413
        |||||||

OY      183 lacagtggcggtccgcgcgagcttcacatgtcgtagtagtaacacctcgcaactggaga 242
        |||||||
DB      414 TACAGTGGCGGTCCGCCAGCTTCATTGCGTAGTAACTCGCAACTGAGAGA 473
        |||||||

OY      243 gcgggcgggccacgcgcgttaaacacccaacttcgaattgttaacctcgatagtagga 302
        |||||||
DB      474 GCGGCGGCGGCGCGCGTAAACACCCAACTTCTGAAGTTGACCTGGAATCAGTAGGA 533
        |||||||

OY      303 ataccgcgtgaactaa 319
        |||||||
DB      534 ATACCGCGTGAACCTTAA 550
        |||||||

RESULT 4
AF178401      550 bp      DNA      linear      PLN 20-DEC-2001
LOCUS
DEFINITION Nectria haematococca mpiv strain NRRL22277 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION
VERSION      AF178401
KEYWORDS
SOURCE
ORGANISM      Nectria haematococca mpiv.
                Nectria haematococca mpiv.
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                Hypocreales; Nectriaceae; Nectria.
REFERENCE
AUTHORS      O'Donnell, K.
TITLE      Molecular phylogeny of the Fusarium solani species complex
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 550)
AUTHORS      O'Donnell, K.
TITLE      Direct Submission
JOURNAL      Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA,
                ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES
source
/organism="Nectria haematococca mpiv"
/strain="NRRL22277"
/db_xref="taxon:135211"
/note="forma_specialis: xanthoxyli; anamorph: Fusarium
solani f. sp. xanthoxyli"
<1..>550
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
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BASE COUNT      138 a      158 c      137 g      117 t
ORIGIN

Query Match      93.6%; Score 298.6; DB 8; Length 550;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY      3 aaatcgataaagtaatgtgaattgcgaattcgaatcgaatcgaattcgaagcaca 62
        |||||||
DB      235 AAATCGATAAGTAATGTAATGTGAGAAATGCAATCATCGAATCTTTAAACGCACA 294
        |||||||

OY      63 ttggccggccagatatttcggcgaggatcctgttcgagcgtcattacaccccaaggcc 122
        |||||||
DB      295 TTGCGCCGCCAGTATTTGGCGGCGATGCTGTTCGACGTCATTACAACTCTCAGGCC 354
        |||||||

OY      123 cccgggcttggcgttgggagtcgagcagcccccctcgcgagcacaacgcccccaaa 182
        |||||||
DB      355 CCGGGGCTGGCGTTGGGGATCGCGGAGCCGCCCTCGGGGCAC-ACGCCGTCCCTTAA 413
        |||||||

OY      183 lacagtggcggtccgcgcgagcttcacatgtcgtagtagtaacacctcgcaactggaga 242
        |||||||
DB      414 TACAGTGGCGGTCCGCCAGCTTCATTGCGTAGTAACTCGCAACTGAGAGA 473
        |||||||

OY      243 gcgggcgggccacgcgcgttaaacacccaacttcgaatgttgacctggaatcagtagga 302
        |||||||
DB      474 GCGGCGGCGGCGCGCGTAAACACCCAACTTCTGAAGTTGACCTGGAATCAGTAGGA 533
        |||||||

OY      303 ataccgcgtgaactaa 319
        |||||||
DB      534 ATACCGCGTGAACCTTAA 550
        |||||||

RESULT 5
AF129104      569 bp      DNA      linear      PLN 25-MAR-1999
LOCUS
DEFINITION Nectria haematococca 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.
ACCESSION
VERSION      AF129104
KEYWORDS
SOURCE
ORGANISM      Nectria haematococca.
                Nectria haematococca.
                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                Hypocreales; Nectriaceae; Nectria.
REFERENCE
AUTHORS      Min, B.R.
TITLE      Direct Submission
JOURNAL      Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji
                Dong, Chung Ro-gu, Seoul 110-743, Korea
FEATURES
source
/organism="Nectria haematococca"
/db_xref="taxon:140110"
/note="submitted as Fusarium solani"
<1..>30
/product="18S ribosomal RNA"
31..182
/note="ITS-1"
/product="internal transcribed spacer 1"
183..340
/product="5.8S ribosomal RNA"
341..511
/note="ITS-2"
/product="internal transcribed spacer 2"
512..>569
/product="28S ribosomal RNA"
BASE COUNT      151 a      157 c      140 g      121 t
ORIGIN
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Query Match	93.6%	Score 298.6	DB 8	Length 569
Best Local Similarity	98.4%	Pred. No. 5.1e-72		
Matches 312	Conservative	0	Mismatches 4	Indels 1
OY	3	aaatgcataaagtaatgtcaattgtcagaattcaatgatacatcatgaattcttgaagcaca	62	
Db	234	AAATGGATTAAGTAATGTGTAATTGCGAATTCAGTAAATCATCGAATCTTTGAACGACA	293	
OY	63	ctgcgcgcgcagatattctgcggcgcaatccttgctgaagcgtcatatataaccctcagcc	122	
Db	294	TTGCGCGCCCGCCAGTATTCGGCGGCATGCTGTGTGACGTCATTAACAACCTCAGGCC	353	
OY	123	ccggggccctgcgggttggaatcggggaagccccccgcggcggaacaaagccgtcccca	182	
Db	354	CCCGGCGCTGGCGCTTGGGATGCGGCAAGAGCCCCCTGTGGGACACACGCGTCCGACA	412	
OY	183	tacagtgatgtctccgcgcgcagcttcacattcgttagtaagtaacacctcgaactgaga	242	
Db	413	TACAGTGGCGGTGCCCGCCCGCACGTTCCATGTGGCTAGTACTAACAACCTCGCAACTGAGA	472	
OY	243	ggggcgggcgcaagcgccgtaaacacccaactctgaatgtgaacctcgaaatcagtaga	302	
Db	473	GGCGCGCGGCATGCGGTAAACACCAACTTCTGATGTGACCTCGAATCAGTAGGA	532	
OY	303	ataccgcgtgaactaa 319		
Db	533	ATACCCGCTGAACCTTA 549		
RESULT	6			
AF178397	548 bp	DNA	linear	PLN 20-DEC-2001
LOCUS	AF178397			
DEFINITION	Fusarium ambrosium strain NRRL20438 18S ribosomal RNA gene, partial sequence; Internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.			
ACCESSION	AF178397			
VERSION	AF178397.1			
KEYWORDS	GI:10180238			
SOURCE	Fusarium ambrosium.			
ORGANISM	Fusarium ambrosium.			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.			
AUTHORS	1 (bases 1 to 548)			
TITLE	O'Donnell,K.			
JOURNAL	Molecular phylogeny of the Fusarium solani species complex			
REFERENCE	2 (bases 1 to 548)			
AUTHORS	O'Donnell,K.			
TITLE	Direct Submission			
JOURNAL	Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA			
FEATURES	Location/Qualifiers			
source	1..548			
	/organism="Fusarium ambrosium"			
	/strain="NRRL20438"			
	/db_xref="taxon:131363"			
	<1..>548			
misc_RNA	/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"			
BASE COUNT	141 a 161 c 133 g 113 t			
ORIGIN				
Query Match	93.1%	Score 297	DB 8	Length 548
Best Local Similarity	98.1%	Pred. No. 1.4e-71		
Matches 311	Conservative	0	Mismatches 5	Indels 1
OY	3	aaatgcataaagtaatgtcagaattcaatgatacatcatgaattcttgaagcaca	62	
Db	233	AAATGGATTAAGTAATGTGTAATTGCGAATTCAGTAAATCATCGAATCTTTGAACGACA	292	

Query	Match	Score	DB	Length	549;
63	ttggcgccgcagatgattctggcgggcagtgctggttctgagcgtcatatacaacctcagacc	92.44;	DB 8;	Length 549;	
293	ttggcgccgcagatgattctggcgggcagtgctggttctgagcgtcatatacaacctcagacc	95.68;	Pred. No. 6.4e-71;		
123	cccgagccctggcgtttggagatcggcggaagccccctgcgcggcgacacgcgcgtcccca	0;	Mismatches 14;	Indels 0;	Gaps 0;
353	ccggggcctggcgtttggagatcggcggaagccccctgcgcggcgacacgcgcgtcccca				
183	tacagtggcgttccgcgcgcagcttcattcgtgtagtaagtaaacctcgcgaatggaga				
412	ttacagtggcgttccgcgcgcagcttcattcgtgtagtaagtaaacctcgcgaatggaga				
243	ggcgagccgcgcagcgttggagatcggcggaagccccctgcgcggcgacacgcgcgtcccca				
472	ggcgagccgcgcagcgttggagatcggcggaagccccctgcgcggcgacacgcgcgtcccca				
303	ataccgcgtgaactaa 319				
532	ataccgcgtgaactaa 548				
RESULT 7					
AF178398	549 bp	DNA	linear	PLN 20-DEC-2001	
LOCUS					
DEFINITION	Nectria ipomoeae strain NRRL22101 18S ribosomal RNA gene, partial				
SEQUENCE	sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene,				
VERSION	and internal transcribed spacer 2, complete sequence; and 28S				
KEYWORDS	ribosomal RNA gene, partial sequence.				
ACCESSION	AF178398				
VERSION	AF178398.1 GI:10180239				
SOURCE	Nectria ipomoeae.				
ORGANISM	Nectria ipomoeae.				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
AUTHORS	Hypocreales; Nectriaceae; Nectria.				
TITLE	1 (bases 1 to 549)				
JOURNAL	O'Donnell, K.				
REFERENCE	Molecular phylogeny of the Fusarium solani species complex				
AUTHORS	2 (bases 1 to 549)				
JOURNAL	O'Donnell, K.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA,				
JOURNAL	ARS, 1815 N. University St., Peoria, IL 61604, USA				
FEATURES	Location/Qualifiers				
source	1..549				
	/organism="Nectria ipomoeae"				
	/strain="NRRL22101"				
	/db_xref="taxon:57162"				
	<1..>549				
	/note="contains 18S ribosomal RNA, internal transcribed				
	spacer 1, 5.8S ribosomal RNA, internal transcribed spacer				
	2, and 28S ribosomal RNA"				
BASE COUNT	142 a 158 c 136 g 113 t				
ORIGIN					

OY	183	tacaaatgagcggtccgcggcgaactcttcatttgtagtgaataaaccttcgaactggaga	242
DB	413	TACAACTGGCGGTCCGCGGCAGCTTCATTTGCTAGTACTAACACTTCGCAACTGGAGA	472
OY	243	ggaggcgagccatcgcaaaaaccacaacctctgaatgagttaacctggaatcaggtaaga	302
DB	473	GCGGCGCGGCCATTGGCGTAATAACACCACAATTCTGAATGTTAAGTCACTCGAATCAGTAGGA	532
OY	303	atacccgcgtgaacttaa 319 	
DB	533	ATACCCGCTGAACCTTAA 549	
RESULT	8		
LOCUS	AF178413	546 bp DNA linear	PLN 20-DEC-2001
DEFINITION	Neocosmospora ornamentata strain NRRL22468 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF178413		
VERSION	AF178413.1 GI:10180254		
KEYWORDS	.		
SOURCE	Neocosmospora ornamentata. Neocosmospora ornamentata.		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neocosmospora.		
REFERENCE	1 (bases 1 to 546) O'Donnell,K. Molecular phylogeny of the Fusarium solani species complex unpublished 2 (bases 1 to 546) O'Donnell,K. Direct Submission Submitted (18-AUG-1999) Microbial Properties Research, NCaur, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA		
JOURNAL			
AUTHORS			
TITLE			
FEATURES	Location/Qualifiers		
source	1..546 /organism="Neocosmospora ornamentata" /strain="NRRL22468" /db_xref="taxon:131368"		
misc_RNA	<1..>546 /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"		
BASE COUNT	137 a 157 c 134 g 118 t		
ORIGIN			
Query Match	90.5%; Score 288.6; DB 8; Length 546;		
Best Local Similarity	96.5%; Fred. No. 2.9e-69;		
Matches 306; Conservative	0; Mismatches 9; Indels 2; Gaps 1;		
OY	3	aaatcgataaatgaatgatgcagaatcatggaatcatcgaaatcttgaacgaca	62
DB	233	AAATCGAATAATGATGTAATTCGACAAATTAGTGAATCATCGAATCTTTAAGGCACA	291
OY	63	ttgcgcccgccagatattctgcggcgcatgctgttctgagcgctcataaaccctcagcgc	122
DB	292	TTGCGCCCGCCAGTATTCTGCGGGCATGCCGTTCTGAGCGCTCATTTACAAACCTTCAGGCC	351
OY	123	cgcggagcctcgtggttgggatatcgagggaagcccccttgcygggacaacagcgcccccaaa	182
DB	352	TCCGGGCGCTGGCGTTGGGGATCGGGGGAGCCCCC--GTGGGCACACGCGCTCCCCCAA	409
OY	183	tacaaatgagcggtccgcggcgaactcttcatttgtagtgaataaaccttcgaactggaga	242
DB	410	TACAACTGGCGGTCCGCGGCAGCTTCATTTGCTAGTACTAACACTTCGCAACTGGAGA	469
OY	243	ggaggcgagccatcgcaaaaaccacaacctctgaatgagttaacctggaatcaggtaaga	302
DB	470	GCGGCGCGGCCATTGGCGTAATAACACCACAATTCTGAATGTTAAGTCACTCGAATCAGTAGGA	529

OY	303	ataccgcgtgaacttaa	319
Db	530	ATAACCCGCTGAACCTTAA	546
<hr/>			
RESULT	9		
AF178402			
LOCUS	AF178402	548 bp	DNA linear PLN 20-DEC-2001
DEFINITION	Fusarium sp. NRRL22354	18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.	
ACCESSION	AF178402.1	GI:10180243	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM	Fusarium sp. NRRL22354. Fusarium sp. NRRL22354 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.		
REFERENCE			
AUTHORS	O'Donnell,K.		
TITLE	Molecular phylogeny of the Fusarium solani species complex		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 548)		
AUTHORS	O'Donnell,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA		
FEATURES			
source	location/Qualifiers		
	1..548		
	/organism="Fusarium sp. NRRL22354"		
	/strain="NRRL22354"		
	/db_xref="taxon:131398"		
	<1..>548		
misc_RNA	/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"		
BASE COUNT	139 a 164 c 133 g 112 t		
ORIGIN			
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Query Match	90.3%:	Score 288.2;	DB 8; Length 548;
Best Local Similarity	98.4%:	Pred. No. 3.8e-69;	
Matches 312; Conservative	0;	Mismatches 3;	Indels 2; Gaps 2;
OY	3	aaatgcgaataagtaattgcaattgcagaatcgaatcgaatcgaatcttggaaacgaca	62
Db	234	AAATCGATTAAGTATTGTGAATTCGAGAATTCAGTGATCATCGAATCTTTGAAACGCACA	293
OY	63	ttagcgccgcagcatcttcgycgggcagtgcgttcgagcgatcataccaacctcaggcc	122
Db	294	TTCGCCCGCCGGTATTCGTGGCGGCATGCCGTTCGAGCGTCATTAACACCCTCAGGCC	353
OY	123	cgcggagcttgagtttgggggatcggcggaagcccccttgggggcaaaaagccgctccccc	182
Db	354	CCCCGGCCTGGCGGTGGGGATCGGGG-G-AGCCCCCGGGGGCAC-ACGCCGTCGCCCAA	411
OY	183	tacaagtgcggtlcccgccgacgtctccacltgctgtagtctaacaacaccctcgcaactgaga	242
Db	412	TACAGTGGGGGGTCCGGCGCAGCTTCATTTGGGTGATGACTAACACCTTCGCAAGTGGAGA	471
OY	243	ggcgagcgagccagcgccgttaaaaaccaactctcgaaatgctgaactcgatcaggtagga	302
Db	472	GCGGGCGGCCACGCCGTAACAAACCCCAACTTGTGAAGATTGACCTCGAATCAGTAGAGA	531
OY	303	ataccgcgtgaacttaa	319
Db	532	ATAACCCGCTGAACCTTAA	548
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RESULT	10		
AF178412			

REFERENCE	Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes: Hypocreales; Nectriaceae; Neocosmospora.
AUTHORS	1 (bases 1 to 544)
TITLE	O'Donnell, K. and Gray, L.E. Phylogenetic relationships of the soybean sudden death syndrome pathogen <i>Fusarium solani</i> f. sp. <i>phaseoli</i> inferred from rDNA sequence data and PCR primers for this identification
JOURNAL	Mol. Plant Microbe Interact. 8 (5), 709-716 (1995)
MEDLINE	96025088
FEATURES	
SOURCE	Location/Qualifiers 1..544 /organism="Neocosmospora vasinfecta" /strain="NRRL 22166" /db_xref="taxon:40622"
misc_RNA	1..544 /note="internal transcribed spacer"
BASE COUNT	137 a 157 c 133 g 117 t
ORIGIN	
Query Match	89.5%; Score 285.6; DB 8; Length 544;
Best Local Similarity	96.5%; Pred. No. 2e-68;
Matches 303; Conservative 0; Mismatches 9; Indels 2; Gaps 1;	
Oy	3 aaatgcgaataagtaatgtgaattgcagaattcagtgaaatcgcgaattcttgaaagcaca 62
Db	233 AAATGCGATTAAGTAAATGCAATTCAGAAATTCAGATGATCATCGAATCTTGAACGCACA 292
Oy	63 ttggccggccgacgattcttggcgggcagcgtgttcgagcgtcatctaaacccttcagcgc 122
Db	293 TTGCGCCCGCCAGATATTCCTGGCGGGCATGCTGTTGAGCGTCATTAACCCCTCAGGCC 352
Oy	123 cccggagccttgcggttggggatcgcggagaaagcccccctggcgggcacaaagccgtccccc 182
Db	353 TCCGGGCGCTGGGGGTTGGGGATTCGGGGAGCCGCC - GTGGGCACAGCGCGTCCGCCAAA 410
Oy	183 taacagtgcggttcctccgcgcagcttccattgcgtatgataagaaaccttcgaacttgaga 242
Db	411 TACAATTGGCGGGTCCCGCGCAGCTTCATTCGTGATGATCAACACCTCCGCACTGGGAGA 470
Oy	243 gcggcgccgacgcgcgttaaaacaccacacattctgaattgttgcacgtgaatcagtagaga 302
Db	471 GCGGGCGCGCCACGCGCTAAACACCACTTGTGAATGTTGACCTCGAATCAGTAGAGA 530
Oy	303 ataccgcgtgaact 316
Db	531 ATACCCGCTGAAC 544
RESULT 12	
LOCUS	AF178406 550 bp DNA linear PLN 20-DEC-2001
DEFINITION	Fusarium sp. NRRL22396 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF178406
VERSION	AF178406.1 GI:10180247
KEYWORDS	
SOURCE	Fusarium sp. NRRL22396.
ORGANISM	Fusarium sp. NRRL22396. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE	1 (bases 1 to 550)
AUTHORS	O'Donnell, K.
TITLE	Molecular phylogeny of the <i>Fusarium solani</i> species complex
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 550)
AUTHORS	O'Donnell, K.
TITLE	Direct Submission
JOURNAL	Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES	Location/Qualifiers

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source          1..550  

                /organism="Fusarium sp. NRRL22396"  

                /strain="NRRL22396"  

                /db_xref="taxon:131402"  

misc-RNA  

              <1..>550  

              /note="contains 18S ribosomal RNA, internal transcribed  

              spacer 1, 5.8S ribosomal RNA, internal transcribed spacer  

              2, and 28S ribosomal RNA"  

BASE COUNT      136 a       161 c       133 g       120 t  

ORIGIN  

Query Match      87.8%; Score 280.2; DB 8; Length 550;  

Best Local Similarity 92.7%; Pred. No. 6,1e-67;  

Matches 294; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  

OY    3 aaatgcgaataagtaagtgaattgcaagaattcagtgaatcatcgaaacctttagacgcaca 62  

      |||||  

DB    234 AAATCGGATTACTTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTTGAAACGCCA 293  

OY    63 ttggccgccgcagatattcttgsgggcacatgcctgtctcgagcgcatataaaccttaaggcc 122  

      |||||  

DB    234 TTGGCCCGCCCGCAGTATCTGGCGGCATGCTCTGTCCGACGTCATTACAACCCTCAAGGCC 353  

OY    123 ccgggacccttgacgcttgagggatcgcgcggaagccccctctgscgcacaaacgcgcctcccacaa 182  

      |||||  

DB    354 CCCGGCGCTGGGGCTTGGGGATGCGCGAGAGCCCCCTCGCGCAAACGCCCTCCCCCAA 413  

OY    183 taacaatgacggtccccgcgcagacttcatttgtgtgtgtgtgtacaaaccttcgaactggaga 242  

      |||||  

DB    414 TTTCAATGGCGGGCTCTGCTGCACCTTCATGTGGTGTAGCTAACACTTCGCACAACTGGAAC 473  

OY    243 gcgcgcgcgcgcacgcgcgctaaacaacccaactctctaagtltgaacctgcgaatcaggtlaga 302  

      |||||  

DB    474 GCCGCGTGGCGCATGCGCGTAAAAACCCCACAACTTCGAATGTTGACCTCGGATCAGGTAGA 533  

OY    303 ataaccgctgaacttaa 319  

      |||||  

DB    534 ATACCCGCTGAACCTTAA 550  

RESULT 13  

AF150466  

LOCUS         AF150466             480 bp     DNA           linear   PLN 05-JAN-2001  

DEFINITION   Nectria haematococca strain SUF209 internal transcribed spacer 1,  

              5.8S ribosomal RNA gene, and internal transcribed spacer 2,  

              complete sequence.  

ACCESSION    AF150466  

VERSION      AF150466.1 GI:7650164  

KEYWORDS  

SOURCE  

ORGANISM     Nectria haematococca.  

              Nectria haematococca  

              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  

              Eurocreales; Nectriaceae; Nectria.  

REFERENCE    1 (bases 1 to 480)  

              Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.  

              Phylogenetic analysis of phytopathogenic fungus, Fusarium solani  

              based on the rDNA-rTS region  

              Mycol. Res. 104 (10), 1175-1183 (2000)  

REFERENCE    2 (bases 1 to 480)  

              Suga,H., Hyakumachi,M. and Kageyama,K.  

              Direct Submission  

              Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu  

              University, Gifu 501-1112, Japan  

JOURNAL      Location/Qualifiers  

FEATURES  

            source  

              1..480  

              /organism="Nectria haematococca"  

              /strain="SUF209"  

              /db_xref="taxon:140110"  

              /note="anamorph: Fusarium solani f. sp. radicicola"  

              1..150  

              /product="internal transcribed spacer 1"  

              151..308  

              rRNA

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	misc_RNA	/product="5.8S ribosomal RNA"	
		309 .480	/product="internal transcribed spacer 2"
BASE COUNT	121 a	146 c	116 g 97 t
ORIGIN			
Query Match	87.5%; Score 279; DB 8;	Length 480;	
Best Local Similarity	100.0%; Pred. No. 1.3e-66;		
Matches 279; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	3 aaatcgataagtaagtgaattgaaatgcacgtacagtgatcactgatcttgaagccaca	62	
DB	202 AATACGATAAATAATAGTGAATTGCAGAATTCAGTGAACTCGAATCTTTGAACGCACA	261	
OY	63 ttggccccgccagatatcttcgqcgqgcacgtcgtttcgagcgtcatataaccctcaagcc	122	
DB	262 TTGGCCCCGCCAGTATTTCTGGCGGSCATGCTGTTCGAGCCTCATTAACACCCTCAGGCC	321	
OY	123 ccgcggcctbgcgtttgggagatcgcgcgaagaccacctcgcgggcacaaagcgcgtlcccacaa	182	
DB	322 CCGGGGCGCTGGCGCTTGGGGATCGCGCAAGCCCGCTCGCGGCACAAACCGCTCCGCCAAA	381	
OY	183 taccatgtagtgcctccgcgcgcagcttccatttgtgtatgtgtacaaacctccgaactggaga	242	
DB	382 TACACTGGCGGCTCCGCCGACGCTTCATTTGGTAGTAGTACACCTTCGCAACTGTGAGA	441	
OY	243 gcgcgcgcgcacgcgcgtcaaaccaccaactctaatg	281	
DB	442 GCGGGCGGCGCACGCCGCTAAACACCCAACCTTCGTGAATG	480	
RESULT 14			
AF150467	480 bp DNA	linear	PLN 05-JAN-2001
LOCUS	Nectria haematococca strain SUF210 internal transcribed spacer 1,		
DEFINITION	5.8S ribosomal RNA gene, and internal transcribed spacer 2,		
	complete sequence.		
ACCESSION	AF150467		
VERSION	AF150467.1 GI:7650165		
KEYWORDS	.		
SOURCE	Nectria haematococca.		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
	Hypocreales; Nectriaceae; Nectria.		
REFERENCE	1 (bases 1 to 480)		
AUTHORS	Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.		
TITLE	Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-TTS region		
JOURNAL	Mycol. Res. 104 (10), 1175-1183 (2000)		
REFERENCE	2 (bases 1 to 480)		
AUTHORS	Suga,H., Hyakumachi,M. and Kageyama,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-MAY-1999) Molecular Genetics Research Center, Giftu University, Giftu 501-1112, Japan		
FEATURES	Location/Qualifiers		
source	1..480		
	/organism="Nectria haematococca"		
	/strain="SUF210"		
	/db_xref="taxon:140110"		
	/note="anamorph: Fusarium solani f. sp. radicicola"		
misc_RNA	1..150		
	/product="internal transcribed spacer 1"		
rRNA	151..308		
	/product="5.8S ribosomal RNA"		
misc_RNA	309..480		
	/product="internal transcribed spacer 2"		
BASE COUNT	122 a	146 c	115 g 97 t
ORIGIN			
Query Match	87.5%; Score 279; DB 8;	Length 480;	
Best Local Similarity	100.0%; Pred No. 1.3e-66;		

	Matches	279;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	3	aaatgcatgaat	taatgtaatgtaattgcagaattcga	tgatcatgatgaatctttgaacgaca	62					
Db	202	AAATGCGAATACGTAATGTAATGGAGATTCAGTGAATCATGCAATCTTTGAACGCACA			261					
Oy	63	tltagcgcgcgcagcga	tlctctgcgcgcgcac	tcctctgtctcagcgtcatltaaacccctcagcgc	122					
Db	262	TTTCGCGCCCGCCAGTATTCTGGCGGGCACTCGTTTCAGAGCGTATTACAACCTCTCAGGCG			321					
Oy	123	cccgagccctgcgcgttggggatctgcgcgcgaagccctctcgcgcgcacaacgcgtctcccca			182					
Db	322	CCCGGCGCTCGCGCTTGGGGATCGCGGGAAGCCCTCTCGGGCAACAGCGCTCCCCCA			381					
Oy	183	taacagtcgcgtctccgcgcgcga	ctlcca	ctltgcgtagtac	taaacacctcgcgaactgaga	242				
Db	382	TTACAGTGGCGGTCTCCGCGCGACACTTCCATTCGTAGTAGCTAACACCTCCCACTGTGAGA			441					
Oy	243	gcgcgcgcgcgcgcgcgcgt	ataaacaccaccaactcttcaatg	281						
Db	442	CGCGCCGCGCGCACCGCGTAAACACCCCACTTCTGAATG			480					

LOCUS	DEFINITION	FEATURES
AF440567	480 bp DNA linear	LOCUS AF440567
AF440567	5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	LOCUS AF440567
AF440567	480 bp DNA linear	LOCUS AF440567
AF440567	5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	LOCUS AF440567

ACCESSION AF440567
 VERSION AF440567.1 GI:18034435
 KEYWORDS
 SOURCE
 ORGANISM *Nectria haematococca*.
Nectria haematococca

REFERENCE	1 (bases 1 to 480)
AUTHORS	Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE	Genetic analysis of pathogenic and nonpathogenic <i>Fusarium oxysporum</i>

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Can. J. Bot. (2002) In press
2 (bases 1 to 480)
Bao, J.R., Fravel, D.R. and Lazarovits, G.
Direct Submission
Submitted (29-0C-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave., BARC-West, Beltsville, MD 20705, USA

FEATURES	Location/Qualifiers
SOURCE	1. .480

misc_RNA	1.150
----------	-------

rRNA	151. .308
------	-----------

misc_RNA	309.	.480

/product="Internal transcribed spacer 2"			
BASE COUNT	122 a	146 c	115 g
ORIGIN			97 t

Query match	87.58;	Score 279;	DB 8;	Length 480;
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Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 aaatgcgaacagtaatgtgaattgcagaatccagtgaaacacagatccttgaacgcaca 62
|||||
Db 202 AAATGCGAATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTGAACGCACA 261

Qy 63 ttcgcgcgcgcagatctctgycggygcattgcctgtctgagcgctattacaacctcagcc 122
|||||
Db 262 ttccgccccgcagatattctgcggcgccatgacctgttcgacgcctattacaacctcagcc 322

[illegible]

Search completed: August 21, 2002, 22:09:47
Job time: 14201 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:38 ; Search time 594.49 Seconds

(without alignments)
921.287 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319
Sequence: 1 gaaatgcatgaatgaatgct.....ggaataccgcgtgaactaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_032802.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	20	AAV70850 Internal transcrib
2	244.4	76.6	2293	23	AAAS16211 Fungus genomic DNA
3	241.8	75.8	502	21	AAAS16193 Fusarium sp. MF638
4	240.2	75.3	310	20	AAV70851 Internal transcrib
5	240	75.2	561	19	AAV59009 F. avenaceum inter
6	195.2	61.2	582	18	AAV65100 T. harzianum IMI 3
7	184.8	57.9	569	16	AAV65101 T. harzianum IMI 3
8	183.8	57.6	504	18	AAV705400 Fusarium culmorum
9	183.8	57.6	504	19	AAV59028 F. culmorum intern

10	183.8	57.6	504	19	AAV62591 Fusarium culmorum
11	180.4	56.6	545	19	AAV59030 F. moniliforme int
12	180.4	56.6	545	19	AAV62593 Fusarium monillifor
13	180	56.4	546	19	AAV59007 F. poae internal t
14	180	56.4	546	19	AAV62596 Fusarium poae PCR
15	179.6	56.3	569	18	AAV65099 T. harzianum IMI 3
16	174.8	54.8	503	16	AAV705401 Fusarium graminear
17	174.8	54.8	503	19	AAV59029 F. graminearum int
18	174.8	54.8	503	19	AAV62592 Fusarium graminear
19	171.4	53.7	504	22	AAV508426 Internal transcrib
20	163.6	51.3	615	22	AAV76260 Cordyceps sinensis
21	156.8	49.2	610	20	AAV90111 Phomopsis viticola
22	155	48.6	537	21	AAZ91725 Microdochium nivai
23	154.8	48.5	545	16	AAV705403 Phomopsis viticola
24	145.6	45.6	608	20	AAV90110 Phomopsis viticola
25	138.8	43.5	549	21	AAZ91723 Rosellinia necatri
26	138.8	43.5	549	21	AAZ91724 Rosellinia necatri
27	134.2	42.1	382	21	AAV72783 5.8s rRNA gene seq
28	128.4	40.3	605	20	AAV90108 Eutypella vitis in
29	127.8	40.1	553	21	AAZ91726 Rosellinia necatri
30	127.4	39.9	537	24	ABA01153 Deuteromycetes pol
31	126.6	39.7	365	20	AAV70847 Sequence containin
32	125.8	39.4	617	20	AAV90109 Eutypa lata intern
33	125	39.2	587	19	AAV43269 Sequence of ITS re
34	123.2	38.6	365	20	AAV70849 Sequence containin
35	121.2	38.0	364	20	AAV70846 Fusarium monillifor
36	118	37.0	353	16	AAV705402 Diptelodia gossypina
37	118	37.0	568	20	AAV90112 M. nivale internal
38	115.8	36.3	556	19	AAV59008 Microdochium nivai
39	115.8	36.3	556	19	AAV62594 Guignardia citricia
40	113.8	35.7	640	22	AAH73767 Sequence of ITS re
41	112.4	35.2	597	19	AAV43265 Internal transcrib
42	111.2	34.9	346	20	AAV70868 Internal transcrib
43	111	34.8	526	22	AAV70847 Deuteromycetes pol
44	111	34.8	578	24	ABA01155 Guignardia citricia
45	110.6	34.7	618	22	AAH73768

ALIGNMENTS

RESULT 1	
ID	AAV70850 standard: DNA: 319 Bp.
AAV70850:	
AC	AAV70850:
XX	
XX	26-FEB-1999 (first entry)
DT	
XX	
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX	
KW	Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW	Mucor rouxii; M. racemosus; M. plumbeus; A. fumigatus;
KW	M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Fusarium solani.
XX	
PN	MO9850584-A2.
PD	
XX	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	
PR	02-MAY-1997; 97US-0045400.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX	

```
DR WPI: 1999-034737/03.
XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Asbidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Claim 1: Page 12; 45pp: English.
XX
CC The present sequence represents an internal transcribed spacer 2 (ITS2)
CC and adjacent regions. Probes can be derived from the present sequence
CC which are species-specific. The specification also describes ITS2
CC sequence-derived probes for identifying a species selected from
CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinelloides f. circinelloides, Rhizopus oryzae,
CC R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
CC Asbidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
CC (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
SQ Sequence 319 BP: 77 A; 96 C; 84 G; 62 T; 0 other:

Query Match          100.0%; Score 319; DB 20; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.8e-97;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaaatgcgataagtaattgtaattgcagaattcagtcgaatcgcgaattcttgaacga 60
DB 1 gaaatgcgataagtaattgtaattgcagaattcagtcgaatcgcgaattcttgaacga 60
QY 61 catgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
DB 61 catgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
QY 121 ccccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
DB 121 ccccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
QY 181 aatcagtgccgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
DB 181 aatcagtgccgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
QY 241 gaggcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
DB 241 gaggcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
QY 301 gaataccgcgtgaactaa 319
DB 301 gaataccgcgtgaactaa 319

RESULT 2
AAS16211 standard; DNA: 2293 BP.
XX
AC AAS16211:
XX
DT 29-JAN-2002 (first entry)
XX
XX Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
XX
KW Gibberellin: 18S rRNA: Internal transcribed spacer region: ITS1:
KW ITS2: 5.8S rRNA: LTR-1027; species differentiation: GA_4; GA_3; GA_7;
KW flowering: fruit cell elongation: apple; pear; grape; fruit;
KW russet control: fungus; ds.
XX
OS Gibberella fujikuroi.
XX
FH Key Location/Qualifiers
```

```
FT misc_feature 1..1774
FT /*tag= a
FT /note= "18S rRNA gene"
FT 1775..1921
FT misc_feature
FT /*tag= b
FT /note= "ITS1 region"
FT 1922..2078
FT misc_feature
FT /*tag= c
FT /note= "5.8S rRNA gene"
FT 2079..2243
FT misc_feature
FT /*tag= d
FT /note= "ITS2 region"
FT 2244..2293
FT /*tag= e
FT /note= "28S rRNA gene"

US6287800-B1.
11-SEP-2001.
23-AUG-2000; 2000US-0645073.
31-AUG-1999; 99US-151770P.
(GAL/) GALIA20 J L.
(LERM/) LEE M D.
Gallazzo JL, Lee MD:
WPI: 2001-662197/76.

A new method for producing a mixture of gibberellins from Gibberella
fujikuroi results in high titers of GA4 and GA7 useful to promote
flowering and fruit growth in the fruit growing industry
Example 4: Column 9-12; 7pp: English.

This sequence represents a genomic DNA sequence containing the 18S rRNA
gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
rRNA sequences from a mutant strain of Gibberella fujikuroi (LTR-1027)
of the invention. This region of DNA is highly variable and can be used
for species and strain differentiation. The LTR-1027 mutant produces a
mixture of gibberellins which is at least 70 % GA_4 and GA_7.
Gibberellins GA_4 and GA_7 promote flowering and fruit cell elongation,
and are used by growers of apples, pears and grapes to produce larger
fruits and earlier harvests. The mixture of GA_3, GA_4 and GA_7 achieved
using the method of this invention should be particularly useful in the
apple industry where GA_4 has been found more effective in russet
control and in promoting fruit set. This method produces GA_4 and GA_7
in much higher titers than prior art methods.

SQ Sequence 2293 BP: 596 A; 527 C; 592 G; 578 T; 0 other:

Query Match          76.6%; Score 244.4; DB 23; Length 2293;
Best Local Similarity 88.1%; Pred. No. 5.5e-72;
Matches 280; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 aaaaatgcgataagtaattgtaattgcagaattcgaatcgcgaattcttgaacgaac 61
DB 1971 aaaaatgcgataagtaattgtaattgcagaattcgaatcgcgaattcttgaacgaac 2030
QY 62 atgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 121
DB 2031 atgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2090
QY 122 ccccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 181
DB 2091 ccccgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2143
QY 182 atcagtgccgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 241
DB 2144 atcagtgccgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2203
```

Oy	242	agcggcgcgcgcacgcgcgttaaacaacccaacttcgaatgfttgacctggaatcaggtag	301
Db	2204	cgcgccgcgcgcgcgcgcgttaacccccaacttcgaatgttgacctgcgacagtag	2263
Oy	302	aataccgcgtgaactaa	319
Db	2264	ataccgcgtgaactaa	2281
RESULT	3		
AAA61893			
ID	AAA61893	standard; DNA: 502 BP.	
AC	AAA61893:		
XX			
DT	14-NOV-2000	(first entry)	
XX			
De	Fusarium sp. MF6381	rdna internal transcribed spacer (ITS) region.	
XX			
KW	Ribosomal DNA: rDNA ITS region: Internal transcribed spacer; ATCC 74469;		
KW	HIV integrase inhibitor; steroid compound; human immunodeficiency virus;		
KW	acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;		
KW	symptomatic infection; asymptomatic infection; potential HIV exposure;		
KW	combination therapy; ds.		
XX			
OS	Fusarium sp. MF6381.		
XX			
PN	MO200036132-A1.		
PD	22-JUN-2000.		
XX			
PF	09-DEC-1999; 99MO-US29356.		
PR	14-DEC-1998; 98US-0112168.		
XX			
PA	(MERI) MERCK & CO INC.		
XX			
P1	Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;		
P1	Dombrowski AW;		
XX	WPI: 2000-431606/37.		
XX			
PT	New steroid compounds are HIV integrase inhibitors used for treating		
PT	HIV infection and AIDS -		
XX			
PS	Disclosure: Page 14; 113pp: English.		
XX			
CC	The invention relates to novel steroid compounds derived from the		
CC	African soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as		
CC	inhibitors of HIV integrase. The invention encompasses cultures of		
CC	Fusarium sp. MF6381. The invention also relates to a composition		
CC	comprising a compound of the invention in combination with an AIDS		
CC	antiviral agent, an immunomodulator and an antiinfective agent. The		
CC	compounds of the invention may be used in the inhibition of HIV		
CC	integrase and in the prevention and treatment of HIV infection. A wide		
CC	range of state of HIV infection may be treated: AIDS (acquired		
CC	immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic		
CC	and asymptomatic HIV infection; and actual or potential exposure to HIV.		
CC	The compounds may be used to isolate HIV integrase mutants which are		
CC	potentially useful as screening tools for antiviral compounds. The		
CC	compounds may also be used to establish or determine the site at which		
CC	other antivirals bind to HIV integrase (e.g., by competitive inhibition).		
CC	The present sequence represents the ribosomal DNA (rDNA) internal		
CC	transcribed spacer (ITS) region of Fusarium sp. MF6381, which may be used		
CC	to characterise MF6381.		
XX			
Sequence	502 BP; 127 A; 144 C; 118 G; 113 T; 0 other;		

Query Match	75.88;	Score 241.8;	DB 21;	Length 502;
Best Local Similarity	88.28;	Pred. No. 2.2e-71;		
Matches 276;	Conservative 0;	Mismatches 32;	Indels 5;	Gaps 1

OY	2	aaatgcatgaatgaatgataatggagaattcaatgaatcatcgaaattcttgaacgac	6
Db	195	aaaatgcataatgaataatgataatgcagaattccagtgaaatcatcgaaattcttgaacgac	254
OY	62	atggcccgccagatattctctggcgagatgctgtttcgagcgatcatataacccctcagc	121
Db	255	atggcccgccagatattctctggcgagatgctgtttcgagcgatcatataacccctcagc	314
OY	122	ccccgggcttgcgttttgagatctggcggaagcccccgcgagacaaagccgctcccca	181
Db	315	ccccgggcttgcgttttgagatctggcggaagcccccgcgagacaaagccgctcccca	369
OY	182	atacagtcgagctcccgccgagcttccattgcgtagtgaactaaacctgcgaactgag	241
Db	370	atacagtcgagctcccgccgagcttccattgcgtagtgaactaaacctgcgaactgag	429
OY	242	agcgcgcgagccaaagcgtaaaacacccaacttctgaattgttgaccctcgaaatcgtagg	301
Db	430	agcgcgcgagccaaagcgtaaaacacccaacttctgaattgttgaccctcgaaatcgtagg	489
OY	302	aataccgcgtgaa	314
Db	490	aataccgcgtgaa	502

RESULT	4	
ID	AAV70851	standard; DNA: 310 BP.
AC	AAV70851;	
DT	26-FEB-1999	(first entry)
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.	
XX	Internal transcribed spacer 2; ITS2; probe: <i>Aspergillus flavus</i> ;	
KW	<i>A. niger</i> ; <i>A. terreus</i> ; <i>A. nidulans</i> ; <i>Fusarium solani</i> ; <i>F. moniliforme</i> ;	
KW	<i>Mucor rouxii</i> ; <i>M. racemosus</i> ; <i>M. plumbeus</i> ; <i>M. indicus</i> ; <i>A. fumigatus</i> ;	
KW	<i>M. circinellioideus</i> ; <i>Rhizopus oryzae</i> ; <i>R. microsporus</i> ;	
KW	<i>R. circinans</i> ; <i>R. stolonifer</i> ; <i>Rhizomucor pusillus</i> ; <i>Absidia corymbifera</i> ;	
KW	<i>Cunninghamella elegans</i> ; <i>Pseudallescheria boydii</i> ; <i>Scedosporium apiospermum</i> ;	
KW	<i>Penicillium notatum</i> ; <i>Sporothrix schenckii</i> ; filamentous fungus; ss.	
OS	<i>Fusarium moniliforme</i> .	
XX	WO9850584-A2.	
XX	12-NOV-1998.	
XX	01-MAY-1998; 98WO-US08926.	
XX	02-MAY-1997; 97US-0045400.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PA	Aldorevitch L, Choi JS, Morrison CJ, Reiss E;	
PI	WP1: 1999-034737/03.	
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.	
PT	<i>Aspergillus</i> , <i>Fusarium</i> , <i>Mucor</i> , <i>Rhizopus</i> , <i>Rhizomucor</i> , <i>Absidia</i> ,	
PT	<i>Cunninghamella</i> , <i>Pseudallescheria boydii</i> , <i>Penicillium</i> and <i>Sporothrix</i>	
PT	species.	
XX	Claim 1; Page 12; 45pp; English.	
XX	The present sequence represents an internal transcribed spacer 2 (ITS2)	
CC	and adjacent regions. Probes can be derived from the present sequence	
CC	which are species-specific. The specification also describes ITS2	
CC	sequence-derived probes for identifying a species selected from	
CC	<i>Aspergillus flavus</i> , <i>A. fumigatus</i> , <i>A. niger</i> , <i>A. terreus</i> , <i>A. nidulans</i> ,	
CC	<i>Fusarium solani</i> , <i>F. moniliforme</i> , <i>Mucor rouxii</i> , <i>M. racemosus</i> , <i>M. plumbeus</i>	

XX 07-NOV-1995: 95ES-0002266.
XX (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA (UYSA-) UNIV SALAMANCA.
XX Garcia Ancha I, Grondona Espana I, Monte Vazquez E;
XX WPI: 1997-280728/25.
DR
XX Liquid formulation of Trichoderma harzianum and Trichoderma viride
PT strains - are used as biological control agents against diseases of
XX plants and plant material and as biofertilization agents
XX
PS Disclosure: Page 26; 37pp; Spanish.
XX
XX The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC gene from the filamentous fungi Trichoderma harzianum strain IMI 352940.
CC A novel liquid formulation based on strains of T. harzianum and
CC T. viride, has the following composition (w/v%): 0.1-6 sorbitol;
CC 0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4;
CC 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
CC 0.02-2 manganese; and a biological component comprising at least one of:
CC T. harzianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. harzianum
CC IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352941
CC (3 x 105 to 10 x 107 conidia/ml), T. harzianum CECT 20179 and/or
CC T. viride CECT 20178. The Trichoderma fungi, alone or in combination,
CC are used as gene recipients to increase activity of the formulation as a
CC biological control agent against diseases of plants and plant material
CC and biological entities causing biodegradation, and as a
CC biofertilization (leaching) agent. It is particularly used e.g. in
CC agriculture, forestry and gardening; for controlling microorganisms which
CC damage food and its packaging, construction materials, raw materials and
CC manufactured products. The antagonistic capacity of the four types of
CC T. harzianum and one type of T. viride over other soil fungi makes them
CC useful for control of plant diseases. Use of this formulation allows
CC reduced application of polluting chemical pesticides and is thus more
CC eco-friendly.
XX
XX Sequence 582 BP; 129 A; 178 C; 142 G; 133 T; 0 other;
SO
Query Match 61.2%; Score 195.2; DB 18; Length 582;
Best Local Similarity 83.8%; Pred. No. 1.2e-55;
Matches 266; Conservative 0; Mismatches 48; Indels 4; Gaps 4;
OY 3 aaatgcgataagtaattggaattgcagaattcagtgatcatcgaattccttgagcgaca 62
DB 264 aaatgcgataagtaattggaattgcagaattcagtgatcatcgaattccttgagcgaca 323
OY 63 ttgcgcccgcagatattctggcgggcattcgtttcagcagtcattcaaacctcagggc 122
DB 324 ttgcgcccgcagatattctggcgggcattcgtttcagcagtcattcaaacctcagggc 383
OY 123 ccgagcgctcggttggggatcgcggaagccctcgtggcgacaacgcccgtcccca 182
DB 384 cctccgccc-cctccggttggggatcgcggaagccctcgtggcgacaacgcccgtcccca 442
OY 183 tacagtgagtggtccgcgcgcagcttcattcgttagtagtaaacac-ctcgcaacggag 241
DB 443 tacagtgagtggtccgcgcgcagcttcattcgttagtagtaaacac-ctcgcaacggag 502
OY 242 agcgcgcgcgccac-gcgcgtaaaacacacactctcg-aaattgacatcgaatcagta 299
DB 503 cgcgcgcgcgccacgcttaaacacacactctcgaaatgtagttagctcgatcagta 562
OY 300 ggaatccgcgtaactaa 319
DB 563 ggaatccgcgtaactaa 582

RESULT 7
AAT65101

ID AAT65101 standard; DNA; 569 BP.
XX
XX AAT65101;
AC
XX 17-FEB-1998 (first entry)
DT
XX T. harzianum IMI 352941 5.8 S rRNA gene regions ITS1-ITS4.
DE
XX
XX ITS1-ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzianum;
KM liquid formulation; T. viride; gene recipient; increase activity;
KM biological control agent; plant disease; biodegradation;
KW biofertilization; leaching; ss.
XX
OS Trichoderma harzianum strain IMI 352941.
XX
XX WO9716974-A1.
XX
XX 15-MAY-1997.
PD
XX
XX 06-NOV-1996; 96MO-ES00206.
PF
XX
XX 07-NOV-1995; 95ES-0002266.
PR
XX
XX (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA (UYSA-) UNIV SALAMANCA.
XX
XX Garcia Ancha I, Grondona Espana I, Monte Vazquez E;
XX WPI: 1997-280728/25.
DR
XX
XX Liquid formulation of Trichoderma harzianum and Trichoderma viride
PT strains - are used as biological control agents against diseases of
PT plants and plant material and as biofertilization agents
XX
PS Disclosure: Page 27; 37pp; Spanish.
XX
XX The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC gene from the filamentous fungi Trichoderma harzianum strain IMI 352941.
CC A novel liquid formulation based on strains of T. harzianum and
CC T. viride, has the following composition (w/v%): 0.1-6 sorbitol;
CC 0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4;
CC 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
CC 0.02-2 manganese; and a biological component comprising at least one of:
CC T. harzianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. harzianum
CC IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352941
CC (3 x 105 to 10 x 107 conidia/ml), T. harzianum CECT 20179 and/or
CC T. viride CECT 20178. The Trichoderma fungi, alone or in combination,
CC are used as gene recipients to increase activity of the formulation as a
CC biological control agent against diseases of plants and plant material
CC and biological entities causing biodegradation, and as a
CC biofertilization (leaching) agent. It is particularly used e.g. in
CC agriculture, forestry and gardening; for controlling microorganisms which
CC damage food and its packaging, construction materials, raw materials and
CC manufactured products. The antagonistic capacity of the four types of
CC T. harzianum and one type of T. viride over other soil fungi makes them
CC useful for control of plant diseases. Use of this formulation allows
CC reduced application of polluting chemical pesticides and is thus more
CC eco-friendly.
XX
XX Sequence 569 BP; 139 A; 171 C; 143 G; 116 T; 0 other;
SO
Query Match 57.9%; Score 184.8; DB 18; Length 569;
Best Local Similarity 83.4%; Pred. No. 3.7e-52;
Matches 272; Conservative 0; Mismatches 42; Indels 12; Gaps 5;
OY 3 aaatgcgataagtaattggaattgcagaattcagtgatcatcgaattccttgagcgaca 62
DB 247 aaatgcgataagtaattggaattgcagaattcagtgatcatcgaattccttgagcgaca 306
OY 63 ttgcgcccgcagatattctggcgggcattcgtttcagcagtcattcaaacctcagggc 122
DB 307 ttgcgcccgcagatattctggcgggcattcgtttcagcagtcattcaaacctcagggc 366


```

DT 06-JAN-1999 (first entry)
XX F. moniliforme internal transcribed spacer.
DE
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.
XX Fusarium moniliforme.
OS
XX
FH Key Location/Qualifiers
FT misc_feature 31..178
FT /*tag= a
FT /note= "ITS1"
FT misc_feature 336..488
FT /*tag= b
FT /note= "ITS2"
FT
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 01-AUG-1997; 97US-0905314.
XX
XX 01-AUG-1997; 97US-0905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck Jf:
XX
XX WPI: 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a
PT basis for primers for the species-specific polymerase chain reaction
PT detection of the pathogens
XX
XX Disclosure; Column 23-26: 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat Microdochium and Fusarium fungal
CC pathogens, especially M. nivale, F. graminearum, F. culmorum,
CC F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.
XX
XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 other:
XX
XX
XX Query Match 56.6%; Score 180.4; DB 19; Length 545;
XX Best Local Similarity 82.4%; Pred. No. 1.1e-50;
XX Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;
XX
XX 2 aaatggaataagaatgaatgcagaatcagaatcagaatcagaatcgttgaagcac 61
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 228 aaatgcgaataagaatgaatgcagaatcagaatcagaatcagaatcgttgaagcac 287
XX 62 atggcgccgcgaatcgtgcgggcatcgtgcgttcgagcgctcattacaacctcgaagc 121
DB ||||||||||||||||||||||||||||||||||||||||||||||||
XX 288 atggcgccgcgaatcgtgcgggcatcgtgcgttcgagcgctcattacaacctcgaagc 347
XX 122 ccccgagcctggcgttgggagatcgcggaagccccctgcgggacacagcgctcccccac 181
DB || || || || || || || || || || || || || || || || || || || || || ||
XX 348 ccc--agcttgggttgggagctg-----cagtcctctgcacatcccca 389
XX 182 atacagggcggtgcgcgaatcgttcagtagtagtaaacctcgcgaactggag 241
DB || || || || || || || || || || || || || || || || || || || || || ||
XX 390 ataatctggcggtcagctg--agcttcacacagcgtagtaacttaacacatcgttaccgta 448
XX 242 agcggcgcgccacgcgcgttaaacacacacacacacacacacacacacacacacacacac 301
DB || || || || || || || || || || || || || || || || || || || || || ||
XX 449 atcgtcgcggcgaacgcgttaaac--cccaactctcgaatgttgactcctcgatcagtagg 507

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XX 302 aataccgctgaactaa 319
DB ||||||||||||||||||
XX 508 aataccgctgaactaa 525
XX
XX RESULT 12
XX AAV62593
XX ID AAV62593 standard; DNA; 545 BP.
XX
XX AAV62593:
XX
XX 17-DEC-1998 (first entry)
XX
XX Fusarium moniliforme PCR amplified ITS region DNA sequence.
XX
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
KM Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KM Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
XX Fusarium moniliforme.
XX
XX
XX Key Location/Qualifiers
FH misc_feature 1..30
FT /*tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 31..178
FT /*tag= b
FT /note= "ITS 1"
FT misc_feature 179..335
FT /*tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 336..488
FT /*tag= d
FT /note= "ITS 2"
FT misc_feature 489..545
FT /*tag= e
FT /note= "5' end of large subunit rRNA gene"
XX
XX US5814453-A.
XX
XX 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-0887480.
XX
XX 02-JUL-1997; 97US-0887480.
XX
XX 19-APR-1995; 95MO-US04712.
XX
XX 15-OCT-1996; 96DS-0722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck Jf:
XX
XX WPI: 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
PT sequence - used for detecting fungal pathogens in plant tissue
XX
XX Claim 2; Fig 3; 56pp; English.
XX
XX This represents the DNA sequence of the internal transcribed spacer (ITS)
CC region that was PCR amplified from Fusarium moniliforme. The invention
CC provides a DNA molecule isolated from the ribosomal RNA gene region of a
CC fungal pathogen, where the DNA molecule consists of an ITS sequence
CC selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum,
CC Fusarium moniliforme, Septoria avenae or Microdochium nivale. A method
CC for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
CC F. avenaceum and M. nivale isolates is also provided. The method
CC comprises isolating DNA from a plant leaf infected with at least one of
CC the above pathogens and amplifying parts of the ITS sequence of the
CC pathogen(s) by PCR using specific primers from within these sequences.
CC The pathogen(s) are detected by visualising the amplified part of the
CC ITS sequence.

```



```

FT      /note= "ITS 2*"
FT      misc_feature      490..546
FT      /*tag= "e
FT      /note= "5', end of large subunit rRNA gene"
XX      US5814453-A.
XX      29-SEP-1998.
XX      PD
XX      02-JUL-1997;      97US-0887480.
XX      PP
XX      02-JUL-1997;      97US-0887480.
XX      PR
XX      19-APR-1995;      95MO-US04712.
XX      PR
XX      15-OCT-1996;      96US-0722187.
XX      PA
XX      (NOVS ) NOVARTIS FINANCE CORP.
XX      Beck JJ:
XX      PI
XX      WPI: 1998-541745/46.
XX      DR
XX      DNA isolated from fungal RNA, and its internal transcribed spacer
XX      PT      sequence - used for detecting fungal pathogens in plant tissue
XX      PS
XX      Examples: Columns 87-88; 56pp; English.
XX      CC
XX      This represents the consensus DNA sequence of the internal transcribed
XX      CC      spacer (ITS) region that was PCR amplified from Fusarium poae
XX      CC      isolates, T-427, T-534 and T-756. The invention provides a DNA
XX      CC      molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX      CC      pathogen, where the DNA molecule consists of an ITS sequence selected
XX      CC      from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX      CC      moniliforme, Septoria avenae or Microdochium nivale. A method for
XX      CC      detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
XX      CC      F. avenaceum and M. nivale isolates is also provided. The method
XX      CC      comprises isolating DNA from a plant leaf infected with at least one of
XX      CC      the above pathogens and amplifying parts of the ITS sequence of the
XX      CC      pathogen(s) by PCR using specific primers from within these sequences.
XX      CC      The pathogen(s) are detected by visualising the amplified part of the
XX      CC      ITS sequence.
XX      SO
XX      Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 other:
XX
XX      Query Match      56.4%;      Score 180;      DB 19;      Length 546;
XX      Best Local Similarity 82.4%;      Pred. No. 1.5e-50;
XX      Matches 262;      Conservative 0;      Mismatches 35;      Indels 21;      Gaps
XX
XX      2      aaaaatgcgaataagtatgtgaatctgcagaatccagtgaatcatcgaaatttgaagcac 61
XX      |||||||
XX      230      aaaaatgcgaataagtatgtgaatctgcagaatccagtgaatcatcgaaatttgaagcac 289
XX
XX      62      atgtagccgcgcagatcttgcgcggcagctgtgttcgcgcgtcaattaacccctcgaagc 121
XX      |||||||
XX      290      atgtagccgcgcagatcttgcgcggcagctgtgttcgcgcgtcaattaacccctcgaagc 349
XX
XX      122      ccccgagcctgcgtctggagatcgcgcggaagcccccctgcgggcacaacgcgctcccccac 181
XX      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
XX      350      cc---agcttggtgttgga-----atctgtgtgcacaacagctcccca 390
XX
XX      182      atacagtgtagtgctccgcgcgcagcttccatctgcgtagtagtcaaacactctgcaactgtgag 241
XX      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
XX      DB      391      atgtagtgtagtgctccagctgcg-aggcttcccaagcgtagtagtaattacaacatcgttaatgta 449
XX
XX      242      agcggcgcgcgcgcgcgcgttaaaaccccaactctcgaatgttgacctcgaatcaggttag 301
XX      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
XX      DB      450      atcgtctgcgcgcgcgcgcgttaaac-cccacacttctgaaatgttgacctcgaatcaggttag 508
XX
XX      302      aataccgcgtgaacttaa 319
XX      |||||||
XX      DB      509      aataccgcgtgaacttaa 526

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0Y	63	ttgcgcccgcagtaattcttgcgcggcagtcctgttctcgacgcgtccatcttaaaccccaagcc	122
Dd	247	aaatcgcatgaatacgtcaatgcagaattccagtgacatcatgaattcttgaacgaca	306
QY	3	aaatcgcatgaatgaattgcagaattccagtgacatcatgaattcttgaacgaca	62
QY	3	aaatcgcatgaatgaattgcagaattccagtgacatcatgaattcttgaacgaca	62
DB	247	aaatcgcatgaatacgtcaatgcagaattccagtgacatcatgaattcttgaacgaca	306
QY	63	ttgcgcccgcagtaattcttgcgcggcagtcctgttctcgacgcgtccatcttaaaccccaagcc	122

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:05 ; Search time 5019.06 Seconds
(without alignments)
857,836 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319
Sequence: 1 gaaatcgataaataatgt.....ggaatacccgctgaactaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : EST:*
1: em_estda:*
2: em_esthum:*
3: em_estln:*
4: em_estlnu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_invr:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.8	32.2	214	10	BF251183 EST18443
2	100.2	31.4	213	9	AI209736 c7908a1.f
3	100.2	31.4	318	9	AI213025 y6f0a1.f
4	92	28.8	120	9	AI327878 j0906a1.f
5	92	28.8	141	9	AI327879 j0906a1.f
6	92	28.8	870	12	CNS06K29
7	92	28.8	1004	12	CNS06KGF
8	92	28.8	1043	12	CNS06LUV
9	91.2	28.6	846	12	CNS078E0
10	91.2	28.6	893	12	CNS079EG
11	91.2	28.6	939	12	CNS06KH6
12	91.2	28.6	995	12	CNS07A08
13	91.2	28.6	999	12	CNS07730
14	91.2	28.6	1034	12	CNS079Z2
15	91.2	28.6	1094	12	CNS076RE
16	91.2	28.6	1098	12	CNS07812
17	90.8	28.5	981	12	CNS0769H

C 18	90.4	28.3	360	12	A2923094	A2923094 4908 .gfb7
C 19	90.4	28.3	392	12	A2923588	A2923588 4908 .gfb21
C 20	90.4	28.3	424	12	A2923253	A2923253 4908 .gfb20
C 21	90.4	28.3	436	12	A0874616	A0874616 v111f4.mt
C 22	90.4	28.3	436	12	A0492096	A0492096 v111f4.mt
C 23	90.4	28.3	440	12	A2931033	A2931033 474 .dhz61
C 24	90.4	28.3	448	12	A2916873	A2916873 4911 .fcb3
C 25	90.4	28.3	453	12	A0874719	A0874719 v113f7.mt
C 26	90.4	28.3	456	12	A2923320	A2923320 4908 .gfb20
C 27	90.4	28.3	468	12	A0875362	A0875362 v124b8.mt
C 28	90.4	28.3	480	12	A2931805	A2931805 474 .dhz90
C 29	90.4	28.3	480	12	A0492124	A0492124 v114a10.m
C 30	90.4	28.3	481	12	A0491983	A0491983 v114a12.m
C 31	90.4	28.3	485	12	A0875193	A0875193 v123G12.m
C 32	90.4	28.3	488	12	A2931966	A2931966 474 .dhz92
C 33	90.4	28.3	497	12	A0492076	A0492076 v110D11.m
C 34	90.4	28.3	503	12	A2931107	A2931107 474 .dhz62
C 35	90.4	28.3	505	12	A0875735	A0875735 v128H4.mt
C 36	90.4	28.3	507	12	A0492107	A0492107 v112D10.m
C 37	90.4	28.3	508	12	A2930634	A2930634 474 .dhz56
C 38	90.4	28.3	514	12	A0874657	A0874657 v112D7.mt
C 39	90.4	28.3	515	12	A2927454	A2927454 476 .dlc25
C 40	90.4	28.3	518	12	A2930375	A2930375 474 .dhz53
C 41	90.4	28.3	519	12	A0503306	A0503306 v62C12.mt
C 42	90.4	28.3	520	12	A0874020	A0874020 v101F6.mt
C 43	90.4	28.3	521	12	A0875703	A0875703 v128E11.m
C 44	90.4	28.3	522	12	A0875718	A0875718 v128F5.mt
C 45	90.4	28.3	522	12	A2926778	A2926778 476 .dlc11

ALIGNMENTS

RESULT 1
LOCUS BF251183 214 bp mRNA linear EST 15-NOV-2001
DEFINITION EST18443 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAD94 5' sequence, mRNA sequence.

ACCESSION BF251183
VERSION BF251183.1 GI:16931326
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 214)
AUTHORS Gardner,M.J. and Kirkland,T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source location/Qualifiers
1..214
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAD94"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 46 a 54 c 62 g 52 t
ORIGIN

Query Match 32.2%; Score 102.8; DB 10; Length 214;
Best Local Similarity 84.1%; Pred. No. 2.1e-18;
Matches 116; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy 3 aatgcgataagtaatgtgaattcagaattcagtgaaatcagtaacatttgaacgcaca 62
|||||
Db 14 AAATGCGATTAAGTATGGAATTCGCAATTCGTAATTCGCAATCTTTGAACGCACA 73
Oy 63 ttgcgccccgcaattctgcggcgagcagtcctgttcgagcgatcattacaacctcaggcc 122
|||||
Db 74 ttgcccccttgcgatttcggggcgacatgctgttcgagcgtatcgcaaaccttcgaag 133
Oy 123 ccgggacctgcgttggg 140
|||||
Db 134 CACGCGCTGTGTGTGGG 151

RESULT 2
AI209736/c 213 bp mRNA linear EST 19-OCT-1998
LOCUS
DEFINITION c7g08a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative CDNA lambda zap library Emericella nidulans cDNA clone
c7g08a1 3', mRNA sequence.
ACCESSION
VERSION AI209736
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL
COMMENT Other_ESTs: c7g08a1.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20.
Location/Qualifiers
FEATURES
source 1..213
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="c7g08a1"
/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative CDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 43 a 68 c 63 g 39 t
ORIGIN

Query Match 31.4%; Score 100.2; DB 9; Length 213;
Best Local Similarity 89.3%; Pred. No. 1.1e-17;
Matches 108; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 3 aatgcgataagtaatgtgaattcagaattcagtgaaatcagtaacatttgaacgcaca 62
|||||
Db 202 AACTGCGATTAAGTATGGAATTCGCAATTCGTAATTCGCAATCTTTGAACGCACA 143
Oy 63 ttgcgccccgcaattctgcggcgagcagtcctgttcgagcgatcattacaacctcaggcc 122
|||||
Db 142 ttgcccccttgcgatttcggggcgacatgctgttcgagcgtatcgcaaaccttcgaagcc 83
Oy 123 c 123

Db 82 c 82

RESULT 3
AI213025/c 318 bp mRNA linear EST 19-OCT-1998
LOCUS
DEFINITION y6f01a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative CDNA lambda zap library Emericella nidulans cDNA clone
y6f01a1 3', mRNA sequence.
ACCESSION
VERSION AI213025
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL
COMMENT Other_ESTs: y6f01a1.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 265.
Location/Qualifiers
FEATURES
source 1..318
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="y6f01a1"
/clone_lib="Aspergillus nidulans 24hr asexual
developmental and vegetative CDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 69 a 93 c 88 g 68 t
ORIGIN

Query Match 31.4%; Score 100.2; DB 9; Length 318;
Best Local Similarity 89.3%; Pred. No. 1.3e-17;
Matches 108; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 3 aatgcgataagtaatgtgaattcagaattcagtgaaatcagtaacatttgaacgcaca 62
|||||
Db 204 AACTGCGATTAAGTATGGAATTCGCAATTCGTAATTCGCAATCTTTGAACGCACA 145
Oy 63 ttgcgccccgcaattctgcggcgagcagtcctgttcgagcgatcattacaacctcaggcc 122
|||||
Db 144 ttgcccccttgcgatttcggggcgacatgctgttcgagcgtatcgcaaaccttcgaagcc 85
Oy 123 c 123

Db 84 c 84

RESULT 4
AI327878/c 120 bp mRNA linear EST 28-DEC-1998
LOCUS
DEFINITION j0908a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative CDNA lambda zap library Emericella nidulans cDNA clone
j0908a1 3', mRNA sequence.
ACCESSION
AI327878

[illegible]

FEATURES	620 Parittington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broeseu.edu We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center putative full length read The vector to vector length is 142 Seq primer: T3.			
SOURCE	Location/Qualifiers 1. 141 /organism="Emerlicella nidulans" /strain="FGSC A26" /db.xref="taxon:162425" /clone="j0g06a1" /clone_id="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /tissue_type="vegetative mycelia, asexual structures" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Xho; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"			
BASE COUNT	33 a 34 c 40 g 34 t			
ORIGIN				
Query Match	28.8%; Score 92; DB 9; Length 141;			
Best Local Similarity	90.7%; Pred. No. 1.8e-15;			
Matches	98: Conservative 0; Mismatches 10; Indels 0; Gaps 0;			
Oy	3 aaatcgataagtaatgcygaattgcagaatcgaatcgaatccttgaacgcaca 62 			
Db	31 AACTCGAATAGTATGTAATGCAATGCAGAAATCAGTCAATCATCGATCTTTGAAACGCACA 90 			
Oy	63 ttgcgcgccgcagatattctgcgaggcatgcctgttgcagcgcatcacc 110 			
Db	91 TTGCCCCCTTGCGCATTCGCGGGCGCATGCCGTCCGAGCGTCATTGC 138 			
RESULT 6				
CNS06K29				
LOCUS	CNS06K29 870 bp DNA linear GSS 17-JUN-2001			
DEFINITION	T7 end of clone AT0AA009C05 of library AT0AA from strain CBS 4311			
ACCESSION	T7 end of clone AT0AA009C05 of library AT0AA from strain CBS 4311			
VERSION	AI0403531			
KEYWORDS	AI0403531.1 GI:12163884			
SOURCE	GSS.			
ORGANISM	Saccharomyces servazzii.			
REFERENCE	Saccharomyces servazzii.			
AUTHORS	Saccharomyces servazzii.			
TITLE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
JOURNAL	1 (bases 1 to 870)			
MEDLINE	Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,			
REFERENCE	Artiguenave,F., Wincker,P. and Galliardin,C.			
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 7.			
TITLE	Saccharomyces servazzii			
JOURNAL	PEBS Lett. 487 (1), 47-51 (2000)			
MEDLINE	20584717			
REFERENCE	2 (bases 1 to 870)			
AUTHORS	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,			
TITLE	Boiotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,			
JOURNAL	de-Montigny,J., Dujon,B., Duren,P., Lepingle,A., Lorente,B.,			
MEDLINE	Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,			
REFERENCE	Saurin,W., Tekala,F., Toffano-Nicche,C., Wesolowski-Louvel,M.,			
AUTHORS	Wincker,P. and Weissenbach,J.			
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of			
JOURNAL	yeast species for molecular evolution studies			
MEDLINE	PEBS Lett. 487 (1), 3-12 (2000)			
REFERENCE	20584711			
AUTHORS	3 (bases 1 to 870)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
REFERENCE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
AUTHORS	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,			
TITLE				

This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces fragilis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia anomala*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

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1. .870
/organism="Saccharomyces servazzii"
/strain="CNC 4311"
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	<1..>1004	
	/note="part of rDNA repeats"	
	/evidence=not_experimental	
BASE COUNT	258 a	12 others
	211 c	247 g
		276 t

Query Match	28.8%	Score 92;	DB 12;	Length 1004;
Best Local Similarity	90.7%	Pred. No. 4	1e-15:	

3 aaatgcgataagtaatgtgaattgcgaattcgaatgaatcatcgaaatccttgaacgcaca 62

63 ttgcgccgcagtatcttcgcgcgcatgcctgttcgagcgctattac 110

CNS06KGF	1004 h	run	11:00-11:30	000 12 2000 0001
CNS06KGF				
1004 h				

CNS06LUT	LOCUS	1043 bp	DNA	linear	GSS 17-JUN-2001
CNS06LUT	T7 end of clone XAT0AA001G02 of library XAT0AA from strain CBS 43111				

of *Saccharomyces servazii*
AL404672

VERSION	AL404672.1	GI:12166434
KEYWORDS	GSS.	

SOURCE	ORGANISM
Saccharomyces servazii.	Saccharomyces servazii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycet
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE
1 (bases 1 to 1043)
Casaregola, S., Lepingle, A., Bon, E., Neuvéglise, C., Nguyen, H.,
Artiguenave, F., Winkler, P. and Galliard, C.
Artiguenave, F., Winkler, P. and Galliard, C.

TITLE Genomic exploration of the hemiascomycetous yeasts: 7
Saccharomyces servazii

**JOURNAL
FEBS Lett. 487 (1), 47-51 (2000)
MEDLINE
20584717**

REFERENCE	MODELING
2 (bases 1 to 1043)	20584717
Souciety, J. L., Ajaie	

de-Montigny, J. A. Dutto
Bolotin-Fukuhara, M.,
Bouciuc, S. L., Higley

Saurin, W., Tekaja, E.,
Malpertuy, A., Neuvogt,
de Montigny, C., Dujon

TITLE Genomic exploration of the hemiascomycetous yeasts: 1 A set of
Scahill, M., Yanada, F., Ioliano-Nicche, C., Wesolowski-Douvet, M.,
Wincker, P. and Weissensbach, J.

TITLE
Genomic exploitation of the nematode-specific yeasts: I. A set of yeast species for molecular evolution studies

COUNTNAL	FBS Lett. 48/ (1),
MEDLINE	20584711
REFERENCE	3 (bases 1 to 1043)

REFERENCE
AUTHORS
TITLE
3 (bases 1 to 10
Genoscope.
Direct Submission

FEATURES	source	misc_feature	BASE COUNT	ORIGIN
COMMENT	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvarum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Karwinia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.			
FEATURES	Location/Qualifiers			
source	1..1043			
	/organism="Saccharomyces servazzii"			
	/strain="CBS 4311"			
	/db_xref="taxon:27293"			
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	/note="end : 17"			
	<1..>1043			
	/note="part of rDNA repeats"			
	/evidence="not_experimental"			
BASE COUNT	265 a 213 c 257 g 305 t		3 others	
ORIGIN				
Query Match	28.8% Score 92: DB 12: Length 1043:			
Best Local Similarity	90.7%: Pred. NO. 4.1e-15:			
Matches	98: Conservative 0: Mismatches 10: Indels 0: Gaps 0:			
OY	3 aaatcgaataagtaatggaattgcagaatcagaatcagaatcagaatcgttaacgaca 62			
Db	626 AATGCGATAGCTATATGGAATTCGCAATTCGGTACATCAATCGAATCTTGTAACGACA 685			
OY	63 ttgcgcgcgcagatattctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 110			
Db	686 TTGCGCCCTCTGCTATTCACGGGCGATGCCCTGTTGACGCTCATTTTC 733			
RESULT 9				
CNS07820				
LOCUS	CNS07820 846 bp DNA linear GSS 08-JUL-2001			
DEFINITION	T7 end of clone BB0AA025B03 of library BB0AA from strain CBS 4732			
ACCESSION	AL434652			
VERSION	AL434652.1 GI:12218066			
KEYWORDS	GSS.			
SOURCE	<i>Pichia angusta</i> .			
ORGANISM	<i>Pichia angusta</i> .			
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; <i>Pichia</i> .			
AUTHORS	1 (bases 1 to 846) Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B.			
TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. <i>Pichia angusta</i>			
JOURNAL	FEBS Lett. 487 (1), 76-81 (2000)			
MEDLINE	20584723			
REFERENCE	2 (bases 1 to 846)			
AUTHORS	Souciat, J. L., Aigle, M., Artiguenave, F., Blandin, G., Boivin, F., Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de Montigny, J., Dujon, B., Durans, P., Leplingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozler, K., Papadimitrakopoulos, O., Potier, S., Sarrin, M., Tekala, F., Toffano-Nicche, C., Wesolowski-Louvel, M., Wincker, P., and Weissbach, J.			
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies			
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)			
MEDLINE	20584711			
REFERENCE	3 (bases 1 to 846)			
AUTHORS	Genoscope.			

TITLE	Direct Submission					
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqlife@genoscope.cns.fr - Web : www.genoscope.cns.fr)					
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marianus var. marianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.					
FEATURES	Location/Qualifiers					
SOURCE	1..846					
	/organism="Pichia angusta"					
	/strain="CBS 4732"					
	/db_xref="taxon:4905"					
	/clone="BB0AA025B03"					
	/clone_lib="BB0AA"					
	/note="end : T7"					
misc_feature	<1..>846					
	/note="Part of rDNA repeats					
	contains 35S rDNA"					
	/evidence=not_experimental					
BASE COUNT	224 a	165 c	188 g	267 t	2 others	
ORIGIN						
	Query Match 28.6%; Score 91.2; DB 12; Length 846;					
	Best Local Similarity 82.9%; Pred. No. 6,3e-15;					
	Matches 116; Conservative 0; Mismatches 23; Indels 1; Gaps 1;					
Oy	3	aatgcgataagtaattgaattcagaattcagaatcatcgatcttgaagcacca	62			
Dd	462	AATGCGATAGCTAATGTGAATGCAGATTTCGTGAATCATTTGTAACGCACA	521			
Oy	63	ttagccgccgcagatatttgcgggcagcgcgttcgtcgaagcgtcataaacccctcaggcc	122			
Dd	522	TTGCCGCCCTCGGTATTCACAGGGCAGTCCGTTTGAGCGCATTTTC-CCTCCAACC	580			
Oy	123	cccgggacctgcgctggggga	142			
Dd	581	CTCGGGTTTGTGATGGCA	600			
RESULT 10						
CNS079EG						
LOCUS	CNS079EG	893 bp	DNA	linear	GSS 08-JUL-2001	
DEFINITION	T7 end of clone BB0AA028D03 of library BB0AA from strain CBS 4732					
ACCESSION	AL435182					
VERSION	AL435182.1	GI:12218595				
KEYWORDS	GSS.					
SOURCE	Pichia angusta.					
ORGANISM	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.					
REFERENCE	1 (bases 1 to 893) Blandin,G., Llorente,B., Malpertuy,A., Winkler,P., Artiguenave,F. and Dujon,B. Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta FEBS Lett. 487 (1), 76-81 (2000)					
JOURNAL						
MEDLINE	2 (bases 1 to 893) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boivin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Winkler,P. and Weissenbach,J.					
AUTHORS						

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEMS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 893)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source location/Qualifiers

1..893

/organism="Pichia angusta"

/strain="CBS 4732"

/db_xref="taxon:4905"

/clone="BB0A028D03"

/clone_1lb="BB0AA"

/note="end : T7"

misc_feature <1..>893

/note="part of rDNA repeats contains 35S rDNA"

/evidence="not_experimental"

BASE COUNT 244 a 160 c 226 g 261 t 2 others

ORIGIN

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Best Local Similarity 82.9%; Pred. No. 6.5e-15;

Matches 116; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

OY 3 aaatcgataaagttaattgcaatcagaatcagatcgaatcgaatcttgaagcaca 62

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DB 56 AAATGCGATACGTAAATGTAATTCGATTCGTAATCATGTAATCTTTGAACGCACA 115

OY 63 ttgcgcgcgcagatattctgcgcgcgcgcgtctgttcgcgcgcgcattacaacctcaggcc 122

|||||

DB 116 TTGCGCCCTCTGTAATTCACAGAGGCGCATGCCCTTTGAGCCGCAATTC-CCATCACAAC 174

OY 123 cccggcctgcgcgttgggga 142

|||||

DB 175 CMCGGCTTGTAATGCGCA 194

RESULT 11

CNS06KH6 939 bp DNA 1linear GSS 17-JUN-2001

LOCUS T7 end of clone AT0AA005C05 of library AT0AA from strain CBS 4311

DEFINITION of *Saccharomyces servazzii*, genomic survey sequence.

ACCESSION AL402880

VERSION AL402880.1 GI:12162459

KEYWORDS GSS.

SOURCE *Saccharomyces servazzii*.

ORGANISM *Saccharomyces servazzii*.

REFERENCE 1 (bases 1 to 939)

AUTHORS Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H., Artiguenave,F., Wincker,P. and Gaillardin,C.

TITLE Genomic exploration of the hemiascomycetous yeasts: 7. *Saccharomyces servazzii*

JOURNAL FEMS Lett. 487 (1), 47-51 (2000)

MEDLINE 20584717

REFERENCE 2 (bases 1 to 939)

AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Wetsenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEMS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 939)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source location/Qualifiers

1..939

/organism="Saccharomyces servazzii"

/strain="CBS 4311"

/db_xref="taxon:27293"

/clone="AT0AA005C05"

/clone_1lb="AT0AA"

/note="end : T7"

misc_feature <1..>939

/note="part of rDNA repeats"

/evidence="not_experimental"

BASE COUNT 236 a 198 c 228 g 271 t 6 others

ORIGIN

Query Match 28.6%; Score 91.2; DB 12; Length 939;

Best Local Similarity 88.9%; Pred. No. 6.6e-15;

Matches 96; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 3 aaatcgataaagttaattgcaatcagaatcagatcgaatcgaatcttgaagcaca 62

|||||

DB 647 AAATGCGATACGTAAATGTAATTCGATTCGTAATCATGTAATCTTTGAACGCACA 706

OY 63 ttgcgcgcgcagatattctgcgcgcgcgcgtctgttcgcgcgcgcattacaacctcaggcc 110

|||||

DB 707 TTGCGCCCTCTGTAATTCACAGAGGCGCATGCCCTTTGAGCCGCAATTC-CCATCACAAC 754

RESULT 12

CNS07A08 995 bp DNA 1linear GSS 08-JUL-2001

LOCUS T7 end of clone XBB0AA002E07 of library XBB0AA from strain CBS 4732

DEFINITION of *Pichia angusta*, genomic survey sequence.

ACCESSION AL435966

VERSION AL435966.1 GI:12219379

KEYWORDS GSS.

SOURCE *Pichia angusta*.

ORGANISM *Pichia angusta*.

REFERENCE 1 (bases 1 to 995)

AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F., and Dujon,B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia angusta*

JOURNAL FEMS Lett. 487 (1), 76-81 (2000)

MEDLINE 20584723

REFERENCE	2 (bases 1 to 995)
AUTHORS	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durren,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozler,Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nlliche,C., Wesolowski-Louvel,M., Wincker,P. and Weissbach,J.
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE	20584711
REFERENCE	3 (bases 1 to 995)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES	Location/Qualifiers
SOURCE	1..995 /organism="Pichia angusta" /strain="CBS 4732" /db_xref="taxon:4905" /clone="XBB0A002E07" /clone_1lb="XBB0A" /note="end : T7"
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BASE COUNT	274 a 173 c 242 g 303 t 3 others
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Query Match	28.6% Score 91.2: DB 12: Length 995:
Best Local Similarity	82.9% Pred. No. 6.8e-15;
Matches 116: Conservative	0: Mismatches 23: Indels 1: Gaps 1:
Oy	3 aaatcgataagattgaaatgcagaatcgaatcaacgaactcttgaaaccaca 62
Db	158 AAATGCGATTACTGATTAATGCAATTCAGATTTTTCGTGAATCATTGAACTTTGAACGCACA 217
Oy	63 ttggccgccagcatatcttcggcggaatgacctgttcgagcgcgatcataaacctcaagcc 122
Db	218 TTGGCCGCCCTCTGTGTATTCAGAGGCGATGCCGCTTTGAGCGTCATTTTC-CCTCTCAAACCC 276
Oy	123 ccggaggacctggcggtttgggga 142
Db	277 CTCGGGTTTGCTGATGGCCA 296
RESULT 13	
CNS07730	999 bp DNA linear GSS 08-JUL-2000LOCUS
DEFINITION	T7 end of clone BB0A009A07 of library BB0A from strain CBS 4732
ACCESSION	AL432204
VERSION	AL432204.1 GI:12215618
KEYWORDS	GSS.
SOURCE	Pichia angusta.
ORGANISM	Pichia angusta.
REFERENCE	Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes: Saccharomycetales: Saccharomycetaceae: Pichia. 1 (bases 1 to 999)

AUTHORS		TITLE		JOURNAL		REFERENCE		MEDLINE		AUTHORS	
Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.		Genomic exploration of the hemiascomycetous yeasts: 13. <i>Pichia angusta</i>		FEBS Lett. 487 (1), 76-81 (2000)		2 (bases 1 to 999)		20584723			
Soulier,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boudin-Pichuara,M., Bon,E., Brotter,P., Casaregola,S., de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Llorente,B., Malpertuy,A., Neugeilse,C., Ozler-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nicche,C., Mesolowski-Louvel,M., Wincker,P. and Weissenbach,J.		Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies		FEBS Lett. 487 (1), 3-12 (2000)		3 (bases 1 to 999)		20584711			
Genoscope.		Direct Submission		Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Creteilux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)		This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varium</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbophil</i> a, <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.		Location/Qualifiers			
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<1..>999		/note="end : 77"		/note="part of rDNA repeats contains 35S rDNA"		/evidence-not_experimental		237 a 212 c 235 g 313 t		2 others	
BASE COUNT		237 a 212 c 235 g 313 t		ORIGIN							
misc_feature											
Query Match		28.6% Score 91.2: DB 12: Length 999:									
Best Local Similarity		82.9%: Pred. No. 6.8e-15:									
Matches 116: Conservative		0: Mismatches 23: Indels 1: Gaps 1:									
QY 3 aaatgcataaagtaatgtaattgacagatcagatgtaatcagatcgaatccttgaagcaga 62											
Db 718 AAATGCGATCGTAATGTAATGTCAGATTTTCGTAATCATTTAAATCTTTGAACGCCA 777											
QY 63 ttgcgcgcgcagatattcgc 122											
Db 778 TTGCGCGCTTCGTGTAATTCAGAGGCGCATCGCTGTTGAGCGCTCATTTTC-CCCTCAAAACC 836											
QY 123 cccgcgcctgcgccttgggga 142											
Db 837 CTCGGGTTTGCTGATGGGCA 856											
RESULT 14		CNS07922		1034 bp DNA linear GSS 08-JUL-2001							
LOCUS		T7 end of clone XBBDAA002E02 of library XBBDAA from strain CBS 4733									
DEFINITION		of <i>Pichia angusta</i> , genomic survey sequence.									
ACCESSION		AL435957									
VERSION		AL435957.1		GI:12219370							

	KEYWORD	GSS.
	SOURCE	Pichia angusta.
	ORGANISM	Pichia angusta.
	REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
	AUTHORS	1 (bases 1 to 1034) Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.
	TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta
JOURNAL	FEMS Lett.	487 (1), 76-81 (2000)
MEDLINE	20584723	
REFERENCE	2 (bases 1 to 1034)	
AUTHORS	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Llorente,B., Malpertuy,A., Neugeglise,C., Ozier-Kalogeropoulos,O., Potlier,S., Saurin,M., Tekala,F., Toffano-Nicche,C., Weslowski-Louvel,M., Wincker,P. and Weissenbach,J.	
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies	
JOURNAL	FEMS Lett.	487 (1), 3-12 (2000)
MEDLINE	20584711	
REFERENCE	3 (bases 1 to 1034)	
AUTHORS	Direct Submission	
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : secrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)	
TITLE	This GSS is part of a random genomic sequencing program of fifteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.	
COMMENT	Location/Qualifiers	
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source	/strain="CHS 4732"	
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	/note="end : 77"	
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	/note="part of rDNA repeats contains 35S rDNA"	
	/evidence=not_experimental	
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Query Match	28.6%;	Score 91.2; DB 12; Length 1034;
Best Local Similarity	82.9%;	Pred. No. 6.9e-15;
Matches 116:	Conservative 0; Mismatches 23; Indels 1; Gaps 1;	
OY	3 aaatcgataagtaattgaattgcagaattcaagtgaatcattcgttgaaagcaca	62
DB	498 AAATGCGAATCACTAATGTAATTGCAGATTTTCGTGAACATCATTTGAACGACA	439
OY	63 ttggccgccgcagttatctcgcgaggcatgcccgttcgagcgatcattaaaccttaggc	122
DB	438 TTGGCGCCCTCTGTATTTCCAGAGGAGTCCGTGTTGAGCGTCATTTC-CCTCTCAAAC	380
OY	123 ccggagccctgcgcttggaga	142
DB	379 CTCGGGTTTGATGATGCGCA	360
RESULT	15	

	LOCUS	CNS076RE/c	1094 bp	DNA	linear	GSS 08-JUL-2001
	DEFINITION	T7 end of clone BB0A006D05 of library BB0A from strain CBS 4732				
	ACCESSION	AL431760				
	KEYWORDS	AL431760.1 GI:12215174				
	SOURCE	GSS.				
	ORGANISM	Pichia angusta.				
	REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.				
	AUTHORS	1 (bases 1 to 1094) Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.				
	TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. Pichia				
JOURNAL	MEDLINE	angusta				
REFERENCE	AUTHORS	FEMS Lett. 487 (1), 76-81 (2000)				
		20584723				
		2 (bases 1 to 1094)				
		Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toïfano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.				
	TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
JOURNAL	MEDLINE	FEMS Lett. 487 (1), 3-12 (2000)				
REFERENCE	AUTHORS	20584711				
	TITLE	3 (bases 1 to 1094)				
JOURNAL		Genoscope.				
		Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, Direct Submision				
		2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seql@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
	COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbophilophila, Candida tropicalis and Yarrowia lipolytica. Genomic Inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.				
	FEATURES	Location/Qualifiers				
	source	1..1094				
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		/note="end : T7"				
	misc-feature	<1..>1094				
		/note="part of rDNA repeats contains 35S rDNA" /evidence=not_experimental				
BASE COUNT		336 a 269 c 192 g 293 t				4 others
ORIGIN						
Query Match		28.6% ; Score 91.2; DB 12; Length 1094;				
Best Local Similarity		82.9% ; Pred. No. 7,le-15;				
Matches 116:	Conservative	0; Mismatches 23; Indels 1; Gaps 1;				
Oy	3	aatgcgataagtaattgatcagaattcagtcgaatcatcgaaaccttgaaaggaca 62				
DB	819	AAATGCGATAAGTAATGTAATTCGATTTCCGTGAATCATTTGATTGTAACGCACA 760				
Oy	63	ttagccgccgcagtattctggcgcgagatgccctgttcgagcgcgtcatcaaaccttaggc 122				
DB	759	TTGGCGCCCTCTGTATTCAGAGGCGATGCCGTGTGTGACCGTCAATTTC-CCTCTCAAACG 701				

Oy 123 cccgggcccctggcgttgaggga 142
I IIII IIII IIII I
Db 700 CTCGGGTTTGGTGATGGGCA 681

Search completed: August 21, 2002, 21:32:09
Job time: 12508 sec

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RESULT 2
US-08-905-314A-24
: Sequence 24, Application US/08905314A
: Patent No. 5827695
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5827695artis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 561 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: STRAIN: Fusarium avenaceum
: INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note="3' end of small subunit
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..181
: OTHER INFORMATION: /note="ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 182..338
: OTHER INFORMATION: /note="5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 339..504
: OTHER INFORMATION: /note="ITS 2"
: NAME/KEY: misc_feature
: LOCATION: 505..561
: OTHER INFORMATION: /note="5' end of large subunit
: OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 75.2%; Score 240; DB 1; Length 561;
Best Local Similarity 88.7%; Pred. No. 6,8e-68;
Matches 287; Conservative 2; Mismatches 27; Indels 7; Gaps

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Db	291	ATTGCGCGCCGCTGTGATTCCGGCGGGCATCCGTGTCAGACGTCAATTTCACACCTCAACG	350
QY	122	ccccgcgccttggcgcttggggatctggcggaagccccctggcgcaacaagccgctcccca	181
Db	351	CCCCGGGTTTGTGTTTGGGATTCGGCTCTGCTCTTMTGGCG-----TGCCGCCCCCGAA	404
QY	182	atacagttgctgcctccgcgcgaagcttcatttcgttagtgaatacacctctgcgaacttggag	241
Db	405	ATTACATTGGCGGTCTCGCTGAGCCTCCATTGCGTACTACTAACAACCTCGCAACTGGAA	464
QY	242	agcgagcgagccacgcgcgttaaacacaaccaactctgaattgttaacctcgaatacaagttag	301
Db	465	CGCGCGCGGCGCAATGCGGTAATAAC-CCCAACTTCTGAATTGTGACCTCGGATCAGGTAGG	523
QY	302	ataacgcagctgaactaa	319
Db	524	AATACCGCTGACTTAA	541

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1  RESULT 3
2  US-08-652-127C-6
3  : Sequence 6, Application US/08652127C
4  : Patent No. 5792611
5  :
6  : GENERAL INFORMATION:
7  : APPLICANT: Richard C. Hamelin
8  : TITLE OF INVENTION: DETECTION OF PLANT
9  : TITLE OF INVENTION: PATHOGEN FUNGI
10 : NUMBER OF SEQUENCES: 10
11 :
12 : CORRESPONDENCE ADDRESSES:
13 : ADDRESSEE: George A. Seaby
14 : ADDRESSEE: Seaby & Maclean
15 : STREET: 880 Wellington Street, Suite 708
16 : CITY: Ottawa
17 :
18 : COUNTRY: Canada
19 :
20 : ZIP: K1R 6K7
21 :
22 : COMPUTER READABLE FORM:
23 : MEDIUM TYPE: 3.5 inch diskette
24 : COMPUTER: IBM PC Compatible
25 : OPERATING SYSTEM: PC-DOS/MS-DOS
26 : SOFTWARE: ASCII
27 :
28 : CURRENT APPLICATION DATA:
29 : APPLICATION NUMBER: US/08/652.127C
30 : FILING DATE: May 23, 1996
31 : CLASSIFICATION: 435
32 :
33 : ATTORNEY/AGENT INFORMATION:
34 : NAME: George A. Seaby
35 : REGISTRATION NUMBER: 24,034
36 : REFERENCE/DOCKET NUMBER: 1898
37 : TELECOMMUNICATION INFORMATION:
38 : TELEPHONE: (613) 232-5815
39 : TELEFAX: (613) 232-5631
40 :
41 : INFORMATION FOR SEQ ID NO: 6:
42 : SEQUENCE CHARACTERISTICS:
43 : LENGTH: 581
44 : TYPE: nucleic acid
45 : STRANDEDNESS: double
46 : TOPOLOGY: linear
47 :
48 : US-08-652-127C-6

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Query Match	66.1%	Score 211	DB 1	Length 561
Best Local Similarity	85.5%	Pred. No. 1.4e-58		
Matches 272	Conservative	0	Mismatches 36	Indels 10
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QY	3	aatgcgaataagtaatgtaattgcgaatcaatgcgaatcttgaacgaca	62	
DB	253	AAATCGGAAATGATATGTCGATTTGCGAATTCATCGAATCTTTGAACGCACA	312	

OY 63 ttgagccgcaagatctctgagcgagcgtgtgagcgtcattacaccctcagggc 122
|||||
DB 313 ttgcccgcgcaagatctctgagcgagcgtgtgagcgtcattacaccctcagggc 372
OY 123 ccgagcgctgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 182
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DB 373 ccgagcgctgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 426
OY 183 tacagtgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 242
|||||
DB 427 tttagtgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 483
OY 243 gggagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 301
DB 484 acagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 543
OY 302 aatagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 319
DB 544 aatagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 561

RESULT 4

US-08-652-127C-7

Sequence 7, Application US/08652127C

Patent No. 5792611

GENERAL INFORMATION:

APPLICANT: Richard C. Hamelin

TITLE OF INVENTION: DETECTION OF PLANT

TITLE OF INVENTION: PATHOGEN FUNGI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: George A. Seaby

STREET: 880 Wellington Street, Suite 708

CITY: Ottawa

COUNTRY: Canada

ZIP: K1R 6K7

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,127C

FILING DATE: May 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: George A. Seaby

REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898

TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 232-5815

TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 531

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-652-127C-7

Query Match 65.8%; Score 210; DB 1; Length 531;

Best Local Similarity 85.2%; Pred. No. 2,8e-58;

Matches 271; Conservative 0; Mismatches 37; Indels 10; Gaps 3;

OY 3 aatcgataaagatctctgagcgagcgtgtgagcgtcattacaccctcagggc 62
|||||
DB 203 aatcgataaagatctctgagcgagcgtgtgagcgtcattacaccctcagggc 262
OY 63 ttgagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 122
|||||
DB 263 ttgagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 322

OY 123 ccgagcgctgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 182
|||||
DB 323 ccgagcgctgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 376
OY 183 tacagtgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 242
|||||
DB 377 tttagtgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 433
OY 243 gggagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 301
DB 434 acagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 493
OY 302 aatagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 319
DB 494 aatagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 511

RESULT 5

US-08-652-127C-8

Sequence 8, Application US/08652127C

Patent No. 5792611

GENERAL INFORMATION:

APPLICANT: Richard C. Hamelin

TITLE OF INVENTION: DETECTION OF PLANT

TITLE OF INVENTION: PATHOGEN FUNGI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: George A. Seaby

STREET: 880 Wellington Street, Suite 708

CITY: Ottawa

COUNTRY: Canada

ZIP: K1R 6K7

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,127C

FILING DATE: May 23, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: George A. Seaby

REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898

TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 232-5815

TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 583

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-652-127C-8

Query Match 65.7%; Score 209.6; DB 1; Length 583;

Best Local Similarity 85.5%; Pred. No. 3.9e-58;

Matches 272; Conservative 0; Mismatches 34; Indels 12; Gaps 3;

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DB 257 aatcgataaagatctctgagcgagcgtgtgagcgtcattacaccctcagggc 316
OY 63 ttgagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 122
|||||
DB 317 ttgagcgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 376
OY 123 ccgagcgctgagcgtgtgagcgagcgtgtgagcgtcattacaccctcagggc 182
|||||

Db	377	CCCCGGGCTTGTTGGGGAGATCGCGAGCCCTCCGCGC-----CGCGCTCCCTAA	428
Oy	183	tacagtagcgagtcgccgcgcagcttcacatgagtagtaactaacacctcgcaactgata	242
Db	429	TCTATGTGCGCTCTCGCGTGTAGCTTCTTCGCTGAGTACACACCTTCG---ACTGGAA	485
Oy	243	gcgcgcgcgcgcgcgcgcgctaaacacccaaactctgaatg--ttagacctgaaatcaagtagg	302
Db	486	ACAGCGCGCGCCACCGCCGTTAAACCCCAACTCTGAAAGTTTGACCTCGGATCAGGTAGG	545
Oy	302	ataaccgcctgaacttaa	319
Db	546	AATACCCGCTGAACCTTA	563

```

RESULT 6
US-08-652-127C-5
: Sequence 5, Application US/08652127C
: Patent No. 5792611
:
: GENERAL INFORMATION:
: APPLICANT: Richard C. Hamelin
: TITLE OF INVENTION: DETECTION OF PLANT
: TITLE OF INVENTION: PATHOGEN FUNGI
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: George A. Seaby
: ADDRESSEE: Seaby & Maclean
: STREET: 880 Wellington Street, Suite 708
: CITY: Ottawa
: COUNTRY: Canada
: ZIP: K1R 6K7
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/652.127C
: FILING DATE: May 23, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: George A. Seaby
: REGISTRATION NUMBER: 24,034
: REFERENCE/DOCKET NUMBER: 1898
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 232-5815
: TELEFAX: (613) 232-5831
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 594
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
: US-08-652-127C-5

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Accession	Sequence	Position
Db	CAAAATCTAGTAGGGCGTTCGGCTGATAGCTTCTCTGCTAGTAA--ATACACTCTGGCTCTGG	492
QY	gagagcggcgcgccgaacgtaaacacccaactcttgaat-gttagactctgaatcaag	297
Db	AGTCTGGTGGGGCAGCCCTTAAACCCCAACTTTTTCGTGATGACCTCGAATCAGG	552
QY	tagaatatcccgctgaacttaa	319
Db	TAGGACTACCGCTGAATCTAA	574

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NAME/KEY: misc-feature
LOCATION: 181..337
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FEATURE:
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OTHER INFORMATION: /note= "ITS 2"
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US-08-905-314A-22

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Best Local Similarity 82.4%; Pred. No. 1.2e-48;
Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4

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    |||
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Db 350 CC---AGCTTGGTGTTGGG-----ATCTGTGTGCAAAACACAGTCCCCAA 390
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OY 182 atacagtgagggtgtccgcgcagcttcacatctgcagtgaagcctaaccctgcgaactggag 241
    |||
Db 391 ATTGATTGGGGGTACAGTGTG-AGCTTCCATTACGTAAGTAATTTACACATCTGTTACTGTGA 449
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OY 242 agcggcgcgccacgcgcgcgtaaaacacccaactctgaatgttgacctgaactcagtagc 301
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Db 450 ATGCGTCGGCGCCACGCCGCTTAAC-CCCAACTTGTGAATGTTGACCTGGATCGATCGTAGG 508
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OY 302 aatacccgctgaacttaa 319
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RESULT 15
US-08-887-480-83
; Sequence 83, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; NUMBER OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:

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DB 409 GCGCTCTGCTGCACCTTCATTCGGTAGTAGTAAACCCTGCAACTGATACGGGGCGC 468
OY 241 ggcgaagccgttaaaccccccaactctgaatgtgacctggatcaggttagaataaccg 300
DB 469 GCGCAAGCCGTTAAACCCCACTTGTGAATGTTGACCCTCGATCAGTAGGAATATACCCG 528
OY 301 ctgaac 306
DB 529 CTGAAC 534

RESULT 12

FPJ34558

LOCUS FPJ34558 534 bp DNA linear PLN 15-JUL-1998
DEFINITION Fusarium proliferatum NRRL 22944 internal transcribed spacer RNA.
ACCESSION U34558
VERSION U34558.1 GI:1808934
KEYWORDS
SOURCE
ORGANISM Fusarium proliferatum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE

AUTHORS

TITLE

O'Donnell, K. and Cigelnik, E.
Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous

JOURNAL

MEDLINE

97159566

2 (bases 1 to 534)

O'Donnell, K., Cigelnik, E. and Nirenberg, H.I.

Molecular systematics and phylogeography of the *Gibberella*

fujikuroi species complex

Mycologia 90 (3), 465-493 (1998)

3 (bases 1 to 534)

O'Donnell, K. and Cigelnik, E.

Direct Submision

Submitted (21-AUG-1995) Kerry O'Donnell, NCAUR, USDA, 1815 N.

University St., Peoria, IL 61604, USA

JOURNAL

FEATURES

Location/Qualifiers

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/organism="Fusarium proliferatum"

/strain="NRRL 22944"

/db_xref="taxon:42674"

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misc_RNA

/product="internal transcribed spacer"

BASE COUNT 135 a 149 c 130 g 120 t

ORIGIN

Query Match 97.7% Score 302.8; DB 8; Length 534;
Best Local Similarity 99.3%; Pred. No. 8.4e-83;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aatgcgataaagtaatgtaaatgcaaaatcagtaacatcgaatcttgaacgcaca 60
DB 229 AATGCGATAGTAATGTAATGCAAGATTCAGTAATCAGTAATCTTTGAACGACA 288
OY 61 ttgcgcgcgcagatcttcgagcgagcgcctgctgcagcgtcattcaaccctaaagc 120
DB 289 TTGCGGCCGCCAGTATTCGCGGCGCATGCCCTGTTGAGCCGTCATTTCAACCTCAAGC 348
OY 121 ccgcggttgggttggttggaatcgcaagcccttcgcaagcgcgcgcgcgcgcgcgcgcgc 180
DB 349 CCCGGGTTTGGTGTGGGATCGCGAGCCCTTCGCGCAAGCCGCCCGCAAAATTAAGT 408
OY 181 gcggttcgcgcagcttcacatctgtagtaaaacccctgcgaactgtagcgcgcgcgcgcgc 240
DB 409 GCGGTCTCGCTCAGCTTCATTTGGTAGTAATAAACCTCGCAACTGGTAGCGGCGC 468
OY 241 ggcgaagccgttaaaccccccaactctgaatgtgacctggatcaggttagaataaccg 300
DB 469 GGCCAAGCCGTTAAACCCCACTTGTGAATGTTGACCCTCGATCAGTAGGAATATACCCG 528

OY 301 ctgaac 306
DB 529 CTGAAC 534

RESULT 13

FAU61670

LOCUS FAU61670 534 bp DNA linear PLN 15-JUL-1998
DEFINITION Fusarium annulatum internal transcribed spacer ribosomal RNA.
ACCESSION U61670
VERSION U61670.1 GI:3320344
KEYWORDS
SOURCE
ORGANISM Fusarium annulatum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE

AUTHORS

TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H.I.
Molecular systematics and phylogeography of the *Gibberella*

fujikuroi species complex

Mycologia 90 (3), 465-493 (1998)

2 (bases 1 to 534)

O'Donnell, K., Cigelnik, E. and Nirenberg, H.I.

Direct Submision

Submitted (21-JUN-1996) USDA/ARS/NCAUR, 1815 N. University, Peoria,

IL 61604, USA

JOURNAL

FEATURES

Location/Qualifiers

1..534

/organism="Fusarium annulatum"

/strain="NRRL13614"

/db_xref="taxon:48484"

1..534

misc_RNA

/note="internal transcribed spacer"

BASE COUNT 135 a 148 c 130 g 121 t

ORIGIN

Query Match 97.2% Score 301.2; DB 8; Length 534;
Best Local Similarity 99.0%; Pred. No. 2.6e-82;
Matches 303; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 aatgcgataaagtaatgtaaatgcaaaatcagtaacatcgaatcttgaacgcaca 60
DB 229 AATGCGATAGTAATGTAATGCAAGATTCAGTAATCAGTAATCTTTGAACGACA 288
OY 61 ttgcgcgcgcagatcttcgagcgagcgcctgctgcagcgtcattcaaccctaaagc 120
DB 289 TTGCGGCCGCCAGTATTCGCGGCGCATGCCCTGTTGAGCCGTCATTTCAACCTCAAGC 348
OY 121 ccgcggttgggttggttggaatcgcaagcccttcgcaagcgcgcgcgcgcgcgcgcgcgc 180
DB 349 CCCGGGTTTGGTGTGGGATCGCGAGCCCTTCGCGCAAGCCGCCCGCAAAATTAAGT 408
OY 181 gcggttcgcgcagcttcacatctgtagtaaaacccctgcgaactgtagcgcgcgcgcgcgc 240
DB 409 GCGGTCTCGCTCAGCTTCATTTGGTAGTAATAAACCTCGCAACTGGTAGCGGCGC 468
OY 241 ggcgaagccgttaaaccccccaactctgaatgtgacctggatcaggttagaataaccg 300
DB 469 GGCCAAGCCGTTAAACCCCACTTGTGAATGTTGACCCTCGATCAGTAGGAATATACCCG 528
OY 301 ctgaac 306
DB 529 CTGAAC 534

RESULT 14
LOCUS FSU61693 534 bp DNA linear PLN 17-MAY-2001
DEFINITION Fusarium sp. NRRL25309.
ACCESSION U61693
VERSION U61693.1 GI:3320367
KEYWORDS

REFERENCE	2 (bases 1 to 502)
AUTHORS	Iwen,P.C., Henry,T. and Hinrichs,S.H.
TITLE	Direct Submission
JOURNAL	Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6499, USA
FEATURES	Location/Qualifiers
source	1..502
	/organism="Gibberella fujikuroi"
	/strain="ATCC48843"
	/variety="intermedium"
	/db_xref="ATCC:48843"
	/db_xref="Eaxon:5127"
	/note="anamorph: Fusarium moniliforme"
	1..147
	/note="ITS1"
	/product="Internal transcribed spacer 1"
rRNA	148..304
	/product="5.8S ribosomal RNA"
misc_RNA	305..470
	/product="internal transcribed spacer 2"
rRNA	471.>502
	/product="28S ribosomal RNA"
BASE COUNT	127 a 141 c 121 g 113 t
ORIGIN	
Query Match	97.0% Score 300.8; DB 8; Length 502;
Best Local Similarity	99.3%; Pred. No. 3.5e-82;
Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	1 aaatcgataagtaagtgaattgcgaaattcagaatgacatcatcttgaaagccaca 60
Db	199 AAATCGATAAGTAA.T.T.GCAATTGCACGAATTCAGTAATCATCGAATCTTTGAACGCACA 258
OY	61 ttgcgccgcgcaaglaattctggcgggcacgacctgttcgagcgctcaattcaaccctcaaggcc 120
Db	259 TTGCGCCGCCAGTATCTGTGGCGGCGCATTCTGTCAGAGCGTCAATTTCACACCTCAAGCC 318
OY	121 ccgcggttctgttgttggggatcgagcaagccttcgagcaagccggccccgaactagt 180
Db	319 CCCGGGTTTGTTGGTGGGGATCGGCGAGCCCTTGCGGCGAACCGCCCCGAAATCTAGTG 378
OY	181 gcggtctgcctgcgaactcattgcgttagtagtaaaccctcgcaactgtaagcgcgcc 240
Db	379 GCGGTCCTGCTGCACACTTCCATTGGGTATGTAAACCTCGCAACTGCTACCGCGCGC 438
OY	241 ggccaagccgtltaaaccccccaactcttgaatgttgaccctcgatcaggtagaataccg 300
Db	439 GGCCNAGCCGTTAAACCCCGCAACTTCTGAATCTTGACCTCGGATCAGGTAGGATACC CG 498
OY	301 ctga 304
Db	499 CTGA 502

Search completed: August 21, 2002, 22:09:49
Job time: 14203 sec

Search completed: August 21, 2002, 22:09:49
Job time: 14203 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:40 ; Search time 594.49 Seconds
(without alignments)
895.294 Million cell updates/sec

Title: US-10-046-955-7
310

Sequence: 1 aatgcgataagtaatgtga.....ggaataccgcgtgaactaa 310

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.GeneSeq_032802:*

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- 2: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT:*
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- 4: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT:*
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- 20: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1999.DAT:*
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- 22: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	20 AAV70851	Internal transcrib
2	306.8	99.0	2293	23 AAS16211	Fungus genomic DNA
3	265.8	85.7	502	21 AAV61893	Fusarium sp. MF638
4	249.8	80.6	561	19 AAV59009	F. avenaceum Inter
5	240.2	77.5	319	20 AAV70850	Internal transcrib
6	193.4	62.4	582	18 AAT65100	T. harzianum IMI 3
7	187.6	60.5	546	19 AAV59007	F. poae Internal t
8	187.6	60.5	546	19 AAV62596	Fusarium poae PCR
9	186.6	60.2	504	16 AAT05400	Fusarium culmorum

10	186.6	60.2	504	19 AAV59028	F. culmorum Intern
11	186.6	60.2	504	19 AAV62591	Fusarium culmorum
12	185	59.7	610	20 AAX90111	Phomopsis viticola
13	183.2	59.1	545	19 AAV59030	F. moniliforme Int
14	183.2	59.1	545	19 AAV62593	Fusarium monilifor
15	180.4	58.2	503	16 AAT05401	Fusarium graminear
16	180.4	58.2	503	16 AAV59029	F. graminearum Int
17	180.4	58.2	503	19 AAV62592	Fusarium graminear
18	175	56.5	569	18 AAT65101	T. harzianum IMI 3
19	174.2	56.2	504	22 AAS08426	Internal transcrib
20	168.2	54.3	569	18 AAT65099	T. harzianum IMI 3
21	166.2	53.6	545	16 AAT05403	Microdochium nivai
22	163.8	52.8	608	20 AAX90110	Phomopsis viticola
23	157.8	50.9	537	21 AAZ91725	Rosellinia necatri
24	149.4	48.2	615	22 AAT65260	Cordyceps sinensis
25	147.8	47.7	549	21 AAZ91723	Rosellinia necatri
26	147.8	47.7	549	21 AAZ91724	Rosellinia necatri
27	141.8	45.7	382	21 AAV72783	5.8s rRNA gene seq
28	139	44.8	605	20 AAX90108	Eutypella vitis in
29	137.6	44.4	537	24 ABA01153	Deuteromycetes pol
30	136	43.9	365	20 AAV70847	Sequence containin
31	136	43.9	587	19 AAV43269	Sequence of ITS re
32	136	43.9	617	20 AAX90109	Eutypa lata Intern
33	134.8	43.5	553	21 AAZ91726	Rosellinia necatri
34	131.4	42.4	364	20 AAV70846	Sequence containin
35	126.6	40.8	556	20 AAZ22438	Internal transcrib
36	126	40.6	640	22 AAT73767	Guignardia citrlica
37	125.2	40.4	627	19 AAO94398	P. herpotrichoides
38	125.2	40.4	627	19 AAV62572	P. herpotrichoides
39	125	40.3	309	20 AAV70872	Internal transcrib
40	124.4	40.1	556	19 AAV59008	M. nivale Internal
41	124.4	40.1	556	19 AAV62594	Microdochium nivai
42	124.4	40.1	580	16 AAV43268	Sequence of ITS re
43	123.6	39.9	626	16 AAT05396	P. herpotrichoides
44	123.6	39.9	626	19 AAV62503	P. herpotrichoides
45	123.6	39.9	626	22 AAT75168	Internal transcrib

ALIGNMENTS

RESULT	ID	AAV70851	standard; DNA: 310 BP.
XX	AAV70851		
AC	AAV70851		
XX	26-FEB-1999	(first entry)	
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.		
XX	Internal transcribed spacer 2; ITS2: probe: Aspergillus flavus;		
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;		
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;		
KW	M. circinellioideis; F. circinellioideis; Rhizopus oryzae; R. microsporus;		
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;		
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;		
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.		
XX			
OS	Fusarium moniliforme.		
XX			
PN	W09850584-A2.		
XX	12-NOV-1998.		
PD			
PF	01-MAY-1998;	98WO-US08926.	
XX			
PR	02-MAY-1997;	97US-0045400.	
XX			
PA	(US\$) US DEPT HEALTH & HUMAN SERVICES.		
XX			
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;		

QY 241 ggcgaagcgttaaaccccaactctgaaatgttgacctcgcagtcagtgagaataccg 300
 |||||||
 Db 2212 ggcgaagcgttaaaccccaactctgaaatgttgacctcgcagtcagtgagaataccg 2271
 |||||||
 QY 301 ctgacctaa 310
 |||||||
 Db 2272 ctgacctaa 2281
 |||||||
 RESULT 3
 AAA61893
 ID AAA61893 standard: DNA: 502 BP.
 XX
 AC AAA61893:
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
 XX
 KM Ribosomal DNA: rDNA ITS region: internal transcribed spacer; ATCC 74469;
 KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
 KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
 KM symptomatic infection; asymptomatic infection; potential HIV exposure;
 KM combination therapy; ds.
 XX
 OS Fusarium sp. MF6381.
 XX
 PN WO200036132-A1.
 XX
 PD 22-JUN-2000.
 XX
 PF 09-DEC-1999: 99WO-US29356.
 XX
 PR 14-DEC-1998: 98US-0112168.
 XX
 PA (MER1) MERCK & CO INC.
 XX
 PI Singh SR, Zink DL, Hazuda DJ, Felock PJ, Polishook JD:
 PI Dombrowski AM:
 XX
 DR WPI: 2000-431606/37.
 XX
 PT New steroid compounds are HIV integrase inhibitors used for treating
 PT HIV infection and AIDS -
 XX
 PS Disclosure: Page 14; 113pp: English.
 XX
 CC The invention relates to novel steroid compounds derived from the
 CC African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as
 CC inhibitors of HIV integrase. The invention encompasses cultures of
 CC *Fusarium* sp. MF6381. The invention also relates to a composition
 CC comprising a compound of the invention in combination with an AIDS
 CC antiviral agent, an immunomodulator and an anti-infective agent. The
 CC compounds of the invention may be used in the inhibition of HIV
 CC integrase and in the prevention and treatment of HIV infection. A wide
 CC range of state of HIV infection may be treated: AIDS (acquired
 CC immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic
 CC and asymptomatic HIV infection; and actual or potential exposure to HIV.
 CC The compounds may be used to isolate HIV integrase mutants which are
 CC potentially useful as screening tools for antiviral compounds. The
 CC compounds may also be used to establish or determine the site at which
 CC other antivirals bind to HIV integrase (e.g., by competitive inhibition).
 CC The present sequence represents the ribosomal DNA (rDNA) internal
 CC transcribed spacer (ITS) region of *Fusarium* sp. MF6381, which may be used
 CC to characterise MF6381.
 CC
 XX
 PS Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 other:

Query Match 85.7%: Score 265.8; DB 21; Length 502;
 Best Local Similarity 93.8%: Pred. No. 8,9e-83;
 Matches 288: Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 1 aaatgcgataagtaatgtaaatgtgcaaaatlcagtgaaatcgaatcttgaacgcaca 60
 |||||||
 Db 196 aaatgcgataagtaatgtaaatgtgcaaaatlcagtgaaatcgaatcttgaacgcaca 255
 |||||||
 QY 61 ttgcgccgccgcaatcttctgcgggcacatgctgttcgcagcgatcattcaaccctcaagc 120
 |||||||
 Db 256 ttgcgccgccgcaatcttctgcgggcacatgctgttcgcagcgatcattcaaccctcaagc 315
 |||||||
 QY 121 cccgggttggtgttggggatcgcaagccct--tgcggaagccgggcccgaatctag 178
 |||||||
 Db 316 cccgggttggtgttggggatcgggctgcggtlccaccggtcccgcccgaatctag 375
 |||||||
 QY 179 tggcggtctgcctgcagcttccattgcgtagtaaaacctcgcaactgtgacgcgyc 238
 |||||||
 Db 376 tggcggtctgcctgcagcttccattgcgtagtaaaacctcgcaactgtgacgcgyc 435
 |||||||
 QY 239 ggcgccaagcgttaaaccccaactctgaaatgttgacctcgatcagtgagaatacc 298
 |||||||
 Db 436 ggcgccaagcgttaaaccccaactctgaaatgttgacctcgatcagtgagaatacc 495
 |||||||
 QY 299 cgcctgaa 305
 |||||||
 Db 496 cgcctgaa 502

RESULT 4
 AAV59009
 ID AAV59009 standard: DNA: 561 BP.
 XX
 AC AAV59009:
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE F. avenaceum internal transcribed spacer.
 XX
 KM Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
 KM fungal pathogen Identification; Infection Identification; ss.
 XX
 OS *Fusarium avenaceum*.
 XX
 FH Key Location/Qualifiers
 FH FT misc_feature 31..181
 FT /*tag= a
 FT /note= "ITS1"
 FT 339..504
 FT /*tag= b
 FT /note= "ITS2"
 XX
 PN US5827695-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 01-AUG-1997; 97US-0905314.
 XX
 PR 01-AUG-1997; 97US-0905314.
 XX
 PA (NOVS) NOVARTIS FINANCE CORP.
 XX
 PI Beck JJ:
 PI WPI: 1998-593995/50.
 XX
 DR What pathogen internal transcribed spacer sequences - used as a
 DR PT basis for primers for the species-specific polymerase chain reaction
 PT detection of the pathogens
 XX
 PS Claim 1: Column 29-30; 20pp: English.

This sequence represents an internal transcribed spacer (ITS) sequence of
 the invention. The primer pairs, based on the ITS sequences, are used for
 the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
 pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*,

XX 07-NOV-1995; 95ES-0002266.
PR (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA (UYSA-) UNIV SALAMANCA.
XX Garcia Ancha I, Grondona Espana I, Monte Vazquez E;
XX MPI, 1997-280728/25.
XX
PS Liquid formulation of Trichoderma harzianum and Trichoderma viride
PT strains - are used as biological control agents against diseases of
PT plants and plant material and as bioinhibition agents
XX
PS Disclosure: Page 26; 37pp; Spanish.
XX
XX The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC gene from the filamentous fungi Trichoderma harzianum strain IMI 352940.
CC A novel liquid formulation based on strains of T. harzianum and
CC T. viride, has the following composition (w/v%): 0.1-6 sorbitol;
CC 0.02-2 K3PO3, 0.05-2 KNO3, 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)2HPO4;
CC 0.02-2 manganese; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
CC 0.02-2 manganese; and a biological component comprising at least one of:
CC T. harzianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. harzianum
CC IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352941
CC (3 x 105 to 10 x 107 conidia/ml), T. harzianum CECT 20179 and/or
CC T. viride CECT 20178. The Trichoderma fungi, alone or in combination,
CC are used as gene recipients to increase activity of the formulation as a
CC biological control agent against diseases of plants and plant material
CC and biological entities causing biodegradation, and as a
CC bioinhibition (leaching) agent. It is particularly used e.g. in
CC agriculture, forestry and gardening; for controlling microorganisms which
CC damage food and its packaging, construction materials, raw materials and
CC manufactured products. The antagonistic capacity of the four types of
CC T. harzianum and one type of T. viride over other soil fungi makes them
CC useful for control of plant diseases. Use of this formulation allows
CC reduced application of polluting chemical pesticides and is thus more
CC eco-friendly.
XX
XX Sequence 582 BP; 129 A; 178 C; 142 G; 133 T; 0 other;
SO

ID	AAV59007 standard; DNA; 546 BP.
XX	
AC	AAV59007;
XX	
DT	06-JAN-1999 (first entry)
XX	
DE	F. poae internal transcribed spacer.
XX	
KW	Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM	fungal pathogen identification; infection identification; ss.
XX	
OS	Fusarium poae.
XX	
PH	
FT	Key
FT	misc_feature
FT	Location/Qualifiers
FT	31..169
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FT	/note= "ITS1"
FT	misc_feature
FT	338..489
FT	/tag= "b"
FT	/note= "ITS2"
PN	
XX	US5827695-A.
XX	
PD	27-OCT-1998.
XX	
PX	01-AUG-1997; 97US-0905314.
XX	
PR	01-AUG-1997; 97US-0905314.
XX	
PA	(NOVS) NOVARTIS FINANCE CORP.
PI	
ZI	Beck JJ;
DR	WPI: 1998-59395/50.
XX	
PT	Wheat pathogen internal transcribed spacer sequences - used as a
PT	basis for primers for the species-specific polymerase chain reaction
XX	detection of the pathogens
PS	Claim 1; Column 25-26; 20pp; English.
CC	This sequence represents an internal transcribed spacer (ITS) sequence of
CC	the invention. The primer pairs, based on the ITS sequences, are used for
CC	the PCR amplification detection of wheat Microdochium and Fusarium fungal
CC	pathogens, especially M. nivale, F. graminearum, F. culmorum,
CC	F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC	strains of fungi show different symptoms during infection, which may or
CC	may not be due to infection. Early identification of the strain causing
CC	the infection allows early, and more specific fungicidal treatment.
XX	
SQ	Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 other:
	Query Match 60.5%; Score 187.6; DB 19; Length 546;
	Best Local Similarity 84.5%; Pred. No. 2,1e-55;
	Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4
OY	1 aaatgcatgaatgatgtgaattgcgaataacttaagatcatcgaaattcttgaacgaca 60
DB	211 aaatgcataagaatacttgatcgcagaattcagtgaatcatcgatctttgaacgaca 290
OY	61 ttggccgccgcagatattctgcggcgacatgccttcgcagcgtcatcttaaccccaaggc 120
DB	291 ttggccccgcagatattctgcggcgacatgccttcgcagcgtcatcttaaccccaaggc 350
OY	121 ccggggttggtgtctggggatcgcgaagcccttgcgcgaagcgcggcccgaactagt 180
DB	351 c--agcttgtgtggy-----atctgtgcaaacacacgctccccaattigtgtg 398
OY	181 ggcgttcgctgcagcttcattctggttagttaaacccttcgaacctggttacggcgc 240
DB	399 ggagtcacg-tcagattccatagcgttgaatttaaccacatcgttactggtaatcgtgc 457

Oy 241 ggcacagcgcgttaacccccaactcttcgaagtgtgacctcgatcaagtgatgaataccg 3007
 Db 458 ggcacagcgcgttaaa-cccccaactcttcgaagtgtgacctcgatcaagtgatgaataccg 516
 Oy 301 ctgaacttaa 310
 Db 517 ctgaacttaa 526

Result	8
AAV62596	standard; DNA: 546 BP.
AAV62596:	
17-DEC-1998	(first entry)
Fusarium poae	PCR amplified ITS region consensus DNA sequence.
Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen; Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant; Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum	
PCB; nucleic acid detection; ss.	
Fusarium poae.	
Key	Location/Qualifiers
misc_feature	1..30
misc_feature	/*tag= a
misc_feature	/note= "3' end of small subunit rRNA gene"
misc_feature	31..180
misc_feature	/*tag= b
misc_feature	/note= "ITS 1"
misc_feature	181..337
misc_feature	/*tag= c
misc_feature	/note= "5.8S rRNA gene"
misc_feature	338..489
misc_feature	/*tag= d
misc_feature	/note= "ITS 2"
misc_feature	490..546
misc_feature	/*tag= e
misc_feature	/note= "5' end of large subunit rRNA gene"
US5814453-A.	
29-SEP-1998.	
02-JUL-1997:	97US-0887480.
02-JUL-1997:	97US-0887480.
19-APR-1995:	95MO-US04712.
15-OCT-1996:	96US-0722187.
(NOVS) NOVARTIS FINANCE CORP.	
Beck JJ:	
WPI: 1998-541745/46.	
DNA isolated from fungal RNA, and its internal transcribed spacer sequence - used for detecting fungal pathogens in plant tissue	
Examples: Columns 87-88; 56pp; English.	
This represents the consensus DNA sequence of the internal transcribed spacer (ITS) region that was PCR amplified from Fusarium poae isolates, T-427, T-534 and T-756. The invention provides a DNA molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochium nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided. The method	

CC comprises isolating DNA from a plant leaf infected with at least one of
CC the above pathogens and amplifying parts of the ITS sequence of the
CC pathogen(s) by PCR using specific primers from within these sequences.
CC The pathogen(s) are detected by visualising the amplified part of the
XX ITS sequence.

Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 other;

Query Match	60.5%	Score 187.6;	DB 19;	Length 546;
Best Local Similarity	84.5%;	Pred. No. 2.1e-55;		
Matches 262;	Conservative	0;	Mismatches 34;	Indels 14;
				Gaps 4;

[illegible][illegible]

QY	301	ctgaacttaa	310
Db	517	ctgaacttaa	526

RESULT	9
AAAT054400	
ID	AAAT054400 standard; DNA; 504 BP.
AC	AAAT054400;
XX	
DT	04-JUN-1996 (first entry)
XX	
DE	Fusarium culmorum internal transcribed spacer sequence.
KW	Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KW	Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PER;
KW	Myosphaerella muscicola; amplification; primer; ribosomal RNA gene;
KW	internal transcribed region; strain; capture; colourimetric assay;
KW	isolate; development; population; random amplified polymorphic DNA; ss
XX	
OS	Fusarium culmorum.
PN	WO9529260-A2.
XX	
PD	02-NOV-1995.
XX	
PF	19-APR-1995; 95WO-US04712.
XX	
PR	25-APR-1994; 94US-0233608.
XX	
PA	(CIBA) CIBA GEIGY AG.
XX	
PI	Beck JF, Ligon JM;
XX	
DR	WPI: 1995-383005/49.
XX	
PT	DNA encoding intervening transcribed sequence - used for detection
XX	
PT	of plant fungal pathogens
XX	

PD 27-OCT-1998.

KM Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
KM *Fusarium culmorum*; *Fusarium graminearum*; *Fusarium moniliforme*; plant;
KM *Septoria avenae*; *Microdochium nivale*; *Fusarium poae*; *Fusarium avenaceum*;
KM PCR; nucleic acid detection; ss.

XX	01-AUG-1997:	97US-0905314.
PF		
XX		
PR	01-AUG-1997:	97US-0905314.
XX		
PA	(NOVS) NOVARTIS FINANCE CORP.	
XX		
F1	Beck JJ;	
XX		
DR	WPI; 1998-593995/50.	
XX		
PT	Wheat pathogen internal transcribed spacer sequences - used as a	
PT	basis for primers for the species-specific polymerase chain reaction	
PS	detection of the pathogens	
XX		
PS	Disclosure; Column 21-22; 20pp; English.	
SQ		
Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 4 other:		
Query Match	60.2%; Score 186.6; DB 19; Length 504;	
Best Local Similarity	82.6%; Pred. No. 4.6e-55;	
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3		
QY	I aaagcgatagaatgtagtgcacaaattcagaatcatcgaattcttgaaagccca 60	
DB	212 aaaagcgataagaatgtgatctgcagaatlcagtgaatcatcgaattcttgaaagccaca 271	
QY	61 ttggccccgcagatattctgcggcgcatgccgttcagagcgtcattcaacccttaagcc 120	
DB	272 ttggccccgcagatattctgcggcgcatgccgttcagagcgtcattcaacccttaagcc 331	
QY	121 ccgggttttgttgggtgatatgcgaagcccttcggcgaagccggcccgaactagt 180	
DB	332 c---agcttgytltygg-----agcttgcagltctgctcacctcccacaatacatctg 380	
QY	181 ggcgttcgcgtcgaacctccattcgttagtagtaaaccctgcgaacctgtagcgggcgc 240	
DB	381 ggcgttcgcgtcgaacctccattcgttagtagtaaaccctgcgaacctgtagcgggcgc 440	
QY	241 ggccaagcgtttaaaccccccaactcttgatgttgacctcggatcaggtaggaatacccg 300	
DB	441 ggcyaagccgttaaa--cccgaactcttgatgttgacccctcgatcagtaggaatacccg 499	
QY	301 ctgaa 305	
DB	500 ctgaa 504	
RESULT 11		
AAV62591		
ID	AAV62591 standard; DNA: 504 BP.	
XX		
AC	AAV62591:	
XX		
DT	17-DEC-1998 (first entry)	
XX		
DE	Fusarium culmorum PCR amplified ITS region consensus DNA sequence.	
KM	Internal transcribed spacer: ITS; ribosomal RNA: rRNA; fungal pathogen;	
KM	Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;	
KM	Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;	
KM	PCR; nucleic acid detection; ss.	

[illegible]

OY		181	gcgctcgtcgccgaacttcacatcgtagtgtaagtaaaccctcgcaacctgtagcgggc	240
Dd		381	gcgcgtacgctgraggcttccatacgtagtaatttacatatcyttcacgcygtaatcgtcgc	440
Oy		241	gcccaagccgtttaaaccccccaactctctaagtcttgactcgcatcaggtagaataccc	300
Db		441	ggcycgcgcgctaa-a-cccacaactctgaagtgtyactcgatcaggtagaataccc	499
Oy		301	cctgae 305 	
Db		500	cctgae 504	
		RESULT 12		
ID	AAX90111	standard; DNA: 610 BP.		
AC	AAX90111;			
XX	AAx90111;			
Dt	17-sep-1999	(first entry)		
Xx				
DE	Phomopsis viticola (variant 2) Internal transcribed spacer DNA sequence.			
xx				
KW	ITS1: ITS2: internal transcribed spacer; detection: fungal pathogen;			
xX	gripe; ribosomal RNA gene region; identification: wine; ds.			
OS	Phomopsis viticola.			
Pn	WO929899-A1.			
xx	17-JUN-1999.			
pD	07-dec-1998; 98wo-US25210.			
PF	08-dec-1997; 97us-0986727.			
xx	(GALL-) GALLO WINERY E & J.			
PA	Descenzo RA, Engel SR, Irelan NA:			
PI	WPI; 1999-429921/36.			
DR	Novel primers targeted to internal transcribed spacer region of			
PT	fungal pathogen ribosomal DNA genes			
PS	Disclosure: Page 32; 43pp; English.			
CC	The present invention describes oligonucleotides (I') for identifying			
CC	fungal pathogens, especially of grape plants. The oligonucleotides			
CC	are isolated double stranded nucleic acids representing the internal			
CC	transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the			
CC	organisms Eutypella vitiis, Eutypa lata, Phomopsis viticola or			
CC	Diplodia gossypina. The oligonucleotide are used to detect the fungal			
CC	pathogens, Eutypella vitiis, Eutypa lata, Phomopsis viticola or Diplodia			
CC	gossypina, especially when infecting grape plants. The detection method			
'CC	is used in the wine industry. AAX90075 to AAX90094 represent			
CC	specifically claimed oligonucleotides from the present invention.			
CC	AAX90095 to AAX90105 represent specifically claimed PCR primers for use			
CC	in the detection of the fungal pathogens Eutypella vitiis, Eutypa lata,			
CC	Phomopsis viticola or Diplodia gossypina. The present sequence represents			
CC	an ITS DNA sequence from the present invention.			
SO	Sequence 610 BP; 150 A; 175 C; 163 G; 122 T; 0 other;			
	Query Match 59.7%; Score 185; DB 20; Length 610; Best Local Similarity 83.1%; Pred.No.1.8e-54; Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;			
OY	1	aatcgcataagtaatcggaattgcgaanaattcagtgatcatcgaattcttgaacgcaca	60	
DB	283	aatcgcataagtaatcggaattgcgaattcagtgatcgaattcatcgaattcttgaacgcaca	342	

Oy	61	ttagcgccgagcgaattcttcgcgggcatgacctgttctgagcgatctttcaacccccaagcc	120
Oy			
Db	343	ttgcgccctcttgtaactcggaggacatgcgctgttcgagcgtaatttcaaccccccaag--	400
Oy	121	cccgggtcttgtagttgggatctgcgaagcccttcggcgaaacggcccgcaaatctagt	180
Db	401	-ccgtgccttgcggagatggggacaactgctctcccccgcggggagacaagccctaataaccagtg	459
Oy	181	ggcgtctgcgtcacgcttccalcitgtagtaagtaaaaacccctgcgaacty--gtacgcgac	238
Db	460	ggcagctcgc--caggaccgccgagcgacgtagttaaacccctgcgtccggagggccctgcg	517
Oy	239	gcggcgcaagccgtttaaccccccaacttctgaaTy-ttacctcgatcacgttagaataac	297
Db	518	gtgcctctgcgtttaaccccccaacttctgaaagtttgacctcgatcacgttagaataac	577
Oy	298	ccgcctgaacttaa	310
Db	578	ccgcctgaacttaa	590
 RESULT 13 AAVS9030 ID AAVS9030 standard; DNA; 545 BP.			
XX	AAVS9030:		
AC			
XX			
DT	06-JAN-1999	(first entry)	
XX			
DE	F. moniliforme	internal transcribed spacer.	
KW	Internal transcribed spacer: ITS; Microdochium; Fusarium; wheat pathogen;		
KM	fungal pathogen identification; infection identification; ss.		
XX			
OS	Fusarium moniliforme.		
XX			
FT	Key	Location/Qualifiers	
FT	misc_feature	/..178	
FT		/*tag= a	
FT	misc_feature	/note= "ITS1"	
FT		336..488	
FT		/*tag= b	
FT		/note= "ITS2"	
XX			
XX	US5827695-A.		
PN			
XX			
PD	27-OCT-1998.		
XX			
PF	01-AUG-1997:	97US-0905314.	
XX			
PR	01-AUG-1997:	97US-0905314.	
XX			
PA	(NOVS) NOVARTIS FINANCE CORP.		
PI	Beck JJ:		
DR			
XX	WPI: 1998-593995/50.		
PT			
PT	Wheat pathogen internal transcribed spacer sequences - used as a		
PT	basis for primers for the species-specific polymerase chain reaction		
PT	detection of the pathogens		
PS	Disclosure: Column 23-26: 20pp: English.		
XX			
CC	This sequence represents an internal transcribed spacer (ITS) sequence of		
CC	the invention. The primer pairs, based on the ITS sequences, are used for		
CC	the PCR amplification detection of wheat Microdochium and Fusarium fungal		
CC	pathogens, especially M. nivale, F. graminearum, F. culmorum,		
CC	F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different		
CC	strains of fungi show different symptoms during infection, which may or		
CC	may not be due to infection. Early identification of the strain causing		
CC	the infection allows early, and more specific fungicidal treatment.		

XX	Sequence	545 BP;	148 A;	143 C;	125 G;	129 T;	0 other;
SO	Query Match	59.1%;	Score 183.2;	DB 19;	Length 545;		
	Best Local Similarity	83.5%;	Pred. NO. 7.3e-54;				
	Matches 259;	Conservative 0;	Mismatches 38;	Indels 13;	Gaps 4;		
QY	1 aatcgcataagtaatgtatgtaatctgcaaaaattcaagtgaaatcattcgaatctttgaagcaca	60					
DB	229 aatcgcataagtaatgtatgtaatctgcaaaaattcaagtgaaatcattcgaatctttgaagcaca	288					
QY	61 ttgcgcgccgcagatattctgcgcggcgcataccctcttcgaagcgtcatttcaacctcaagcc	120					
DB	289 ttgcgcgccgcagatattctgcgcggcgcataccctcttcgaagcgtcatttcaacctcaagcc	348					
QY	121 cccgcggattgtgtgttgggagtcgcgaagccctctgcgcgaagccgcgcgaatactagt	180					
DB	349 c--agcttgggtgttgggagtcgcgaagccctctgcgcgaagccgcgcgaatactagt	397					
QY	181 ggcggtctgcctgcagcttccattctgtagtgaataaccctcgcacattgtagcggcgc	240					
DB	398 ggcggtctgcctgcagcttccattctgtagtgaataaccctcgcacattgtagcggcgc	456					
QY	241 ggcgcgaagccgtttaaaccctccttcgattgttgcacctcgcagtaggaataaccg	300					
DB	457 ggcgcgaagccgtttaaaccctccttcgattgttgcacctcgcagtaggaataaccg	515					
QY	301 ctgaacttaa 310						
DB	516 ctgaacttaa 525						
RESULT 14							
AAV62593							
ID	AAV62593 standard; DNA; 545 BP.						
XX	AAV62593;						
AC							
XX							
DT	17-DEC-1998 (first entry)						
XX							
DE	Fusarium moniliforme PCR amplified ITS region DNA sequence.						
XX							
KW	Internal transcribed spacer; ITS; ribosomal RNA; fungal pathogen;						
KW	Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;						
KW	Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;						
KW	PCR; nucleic acid detection; ss.						
XX							
OS	Fusarium moniliforme.						
XX							
FH	Key	Location/Qualifiers					
FT	misc_feature	1..30					
FT		/*tag- a					
FT		/note- "3' end of small subunit rRNA gene"					
FT	misc_feature	31..178					
FT		/*tag- b					
FT		/note- "ITS 1"					
FT	misc_feature	179..335					
FT		/*tag- c					
FT		/note- "5.8S rRNA gene"					
FT	misc_feature	336..488					
FT		/*tag- d					
FT		/note- "ITS 2"					
FT	misc_feature	489..545					
FT		/*tag- e					
FT		/note- "5' end of large subunit rRNA gene"					
XX							
PN	US5814453-A.						
XX							
PD	29-SEP-1998.						
XX							
PF	02-JUL-1997;	97US-00887480.					
XX							

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PR 02-JUL-1997: 97US-0887480.
PR 19-APR-1995: 95MO-US04712.
PR 15-OCT-1996: 96US-0722187.
XX
PA (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ:
PI WPI: 1998-541745/46.
DR
XX DNA isolated from fungal RNA, and its internal transcribed spacer
PT sequence - used for detecting fungal pathogens in plant tissue
XX
XX Claim 2: Fig 3: 56pp: English.
XX
XX This represents the DNA sequence of the internal transcribed spacer (ITS)
CC region that was PCR amplified from Fusarium moniliforme. The invention
CC provides a DNA molecule isolated from the ribosomal RNA gene region of a
CC fungal pathogen, where the DNA molecule consists of an ITS sequence
CC selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum,
CC Fusarium moniliforme, Septoria avenae or Microdochium nivale. A method
CC for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
CC F. avenaceum and M. nivale isolates is also provided. The method
CC comprises isolating DNA from a plant leaf infected with at least one of
CC the above pathogens and amplifying parts of the ITS sequence of the
CC pathogen(s) by PCR using specific primers from within these sequences.
CC The pathogen(s) are detected by visualising the amplified part of the
CC ITS sequence.
XX
XX Sequence 545 BP: 148 A; 143 C; 125 G; 129 T; 0 other:
SO
Query Match 59.1%; Score 183.2; DB 19; Length 545;
Best Local Similarity 83.5%; Pred. No. 7.3e-54;
Matches 259; Conservative 0; Mismatches 38; Indels 13; Gaps 4;
OY 1 aaatgcatagatgaattggaattcaaatcagaatcattcgaattcgaacgaca 60
DB 229 aaatgcatagatgaattggaattcagaatcagaatcagaatcattcgaacgaca 288
OY 61 ttgagccgcagatattctgagcgagatgctgttcagcgatcattcaaccctcaagcc 120
DB 289 ttgagccgcagatattctgagcgagatgctgttcagcgatcattcaaccctcaagcc 348
OY 121 ccgaggttggtgttggtggaatcgcaagcccttcgagcgagcccgcaaatctagt 180
DB 349 c---agcttggtgttggtggtggaatcgcaagcccttcgagcgagcccgcaaatctagt 397
OY 181 gcggtctgcgcagatctcattcagtagtagtaaaacccctcgcaaatctgtaagcgagcc 240
DB 398 gcggtctgcgcagatctcattcagtagtagtaaaacccctcgcaaatctgtaagcgagcc 456
OY 241 ggcacaagcgtttaaaccccaactctgaaatgttgacctggaatcaggtagaatacccg 300
DB 457 ggcacaagcgtttaaa-cccacaactctgaaatgttgacctggaatcaggtagaatacccg 515
OY 301 ctgaacttaa 310
DB 516 ctgaacttaa 525
RESULT 15
AAT05401
ID AAT05401 standard: DNA: 503 BP.
XX
XX AAT05401:
XX
XX 04-JUN-1996 (first entry)
XX
XX Fusarium graminearum internal transcribed spacer sequence.
DE
XX Plant pathogen: fungus: Septoria nodorum; Septoria tritici; Fusarium;
KM Pseudocercospora; herpotrichoides; Mycosphaerella fijiensis; PCR;
```

```
KM Mycosphaerella muscolola; amplification: primer: ribosomal RNA gene;
KM internal transcribed region: strain: capture: colourimetric assay;
KM isolate: development; population; random amplified polymorphic DNA; ss.
XX
XX Fusarium graminearum.
OS
XX MO9529260-A2.
XX
XX 02-NOV-1995.
XX
XX 19-APR-1995: 95MO-US04712.
XX
XX 25-APR-1994: 94US-0233608.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Beck JJ, Ligon JM;
PI WPI: 1995-383005/49.
XX
XX DNA encoding intervening transcribed sequence - used for detection
PT of plant fungal pathogens
XX
XX Claim 1: Page 55: 65pp: English.
XX
XX A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,
CC Mycosphaerella fijiensis, M. muscolola or Fusarium spp. involves the PCR
CC amplification of sequences found in the internal transcribed region
CC (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers
CC AAQ94359-93 and AAT05357-72. These primers are derived from the ITS
CC sequences of these fungi (AAT05394-T05404 and AAQ94398) and are strain
CC specific. The amplification products of the reactions using these
CC primers can be used with the capture primers AAT05378-93 in
CC colourimetric assays. The primers and ITS DNAs can be used for the
CC detection of specific fungal pathogen isolates and in monitoring disease
CC development in plant populations.
XX
XX Sequence 503 BP: 131 A; 127 C; 108 G; 116 T; 21 other:
SO
Query Match 58.2%; Score 180.4; DB 16; Length 503;
Best Local Similarity 80.0%; Pred. No. 6.8e-53;
Matches 248; Conservative 12; Mismatches 38; Indels 12; Gaps 4;
OY 1 aaatgcatagatgaattggaattcaaatcagaatcattcgaattcgaacgaca 60
DB 206 aaatgcatagatgaattggaattcagaatcagaatcagaatcattcgaacgaca 265
OY 61 ttgagccgcagatattctgagcgagatgctgttcagcgatcattcaaccctcaagcc 120
DB 266 ttgagccgcagatattctgagcgagatgctgttcagcgatcattcaaccctcaagcc 325
OY 121 ccgaggttggtgttggtggaatcgcaagcccttcgagcgagcccgcaaatctagt 180
DB 326 c---agttggtgtgtgtggtggaatcgcaagcccttcgagcgagcccgcaaatctagt 375
OY 181 gcggtctgcgcagatctcattcagtagtagtaaaacccctcgcaaatctgtaagcgagcc 240
DB 376 gcggtctgcgcagatctcattcagtagtagtaaaacccctcgcaaatctgtaagcgagcc 434
OY 241 ggcacaagcgtttaaaccccaactctgaaatgttgacctggaatcaggtagaatacccg 300
DB 435 ggcacaagcgtttaaa-cccacaactctgaaatgttgacctggaatcaggtagaatacccg 493
OY 301 ctgaacttaa 310
DB 494 ctgaacttaa 503
Search completed: August 21, 2002, 22:22:42
Job time: 5782 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:09 ; Search time 5019.06 Seconds
(without alignments)
833.633 Million cell updates/sec

Title: US-10-046-955-7
Perfect score: 310
Sequence: 1 aaatgcgataagtaagtga.....ggaataccgcgtgaactaa 310

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hnc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109.2	35.2	214	10	BF251183 EST418443
2	100.8	32.5	213	9	A1209736 c7908a1.f
3	100.8	32.5	318	9	A1213025 y6f0a1.f
4	97.6	31.5	846	12	CNS07820 AL434652 T7 end of
5	97.6	31.5	893	12	CNS07820 AL435182 T7 end of
6	97.6	31.5	995	12	CNS07820 AL435966 T7 end of
7	97.6	31.5	999	12	CNS07820 AL432204 T7 end of
8	97.6	31.5	1034	12	CNS07820 AL435957 T7 end of
9	97.6	31.5	1094	12	CNS07820 AL431760 T7 end of
10	97.6	31.5	1098	12	CNS07820 AL433404 T3 end of
11	97.2	31.4	981	12	CNS07820 AL431115 T7 end of
12	96.4	31.1	522	12	A2927454 476.d1s11
13	96.4	31.1	870	12	A2926778 AL403551 T7 end of
14	96.2	31.0	1004	12	CNS06K29 AL402853 T3 end of
15	96.2	31.0	1043	12	CNS06K29 AL404672 T7 end of
16	96.2	31.0	638	10	BE337372 BE337372 894045B04
17	96	31.0			

18	96	31.0	969	12	CNS07DPM AL439868 T7 end of
19	96	31.0	971	12	CNS07DPL AL440767 T3 end of
20	96	31.0	982	12	CNS07D5J AL440045 T3 end of
21	96	31.0	994	12	CNS07CUT AL439664 T3 end of
22	96	31.0	1014	12	CNS07C17 AL439205 T7 end of
23	96	31.0	1027	12	CNS07DYS AL441098 T3 end of
24	96	31.0	1042	12	CNS07CH2 AL443919 T3 end of
25	96	31.0	1052	12	CNS07DPT AL440775 T3 end of
26	96	31.0	1110	12	CNS07EB9 AL441547 T3 end of
27	95.6	30.8	1010	12	CNS07C1H AL438603 T7 end of
28	95.6	30.8	1029	12	CNS07AHC AL436582 T7 end of
29	95.4	30.8	939	12	CNS06KH6 AL440288 T7 end of
30	94.8	30.6	440	12	A2931033 474.dhz61
31	94.8	30.6	480	12	A2931805 474.dhz30
32	94.8	30.6	503	12	A2931107 474.dhz62
33	94.8	30.6	508	12	A2930634 474.dhz56
34	94.8	30.6	518	12	A2930375 474.dhz53
35	94.4	30.5	1009	12	CNS07DE3 AL440353 T3 end of
36	93.8	30.3	1025	12	CNS06XGS AL441974 T3 end of
37	93.6	30.2	1037	12	CNS06OXE AL408648 T7 end of
38	93.4	30.1	900	12	CNS06ZGK AL422298 T7 end of
39	93.4	30.1	929	12	CNS06UDM AL416190 T7 end of
40	93	30.0	675	12	CNS06Y1Q AL421080 T7 end of
41	93	30.0	725	12	CNS06XRL AL421083 T3 end of
42	93	30.0	823	12	CNS06Y58 AL420594 T3 end of
43	93	30.0	867	12	CNS06Z9V AL422057 T3 end of
44	93	30.0	879	12	CNS06Y5H AL420603 T7 end of
45	93	30.0	896	12	CNS06YXF AL421609 T7 end of

ALIGNMENTS

RESULT 1
LOCUS BF251183 214 bp mRNA linear EST 15-NOV-2001
DEFINITION EST418443 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAD94 5' sequence, mRNA sequence.

ACCESSION BF251183
VERSION BF251183.1 GI:16931326

KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.

REFERENCE 1 (bases 1 to 214)
Gardner,M.J. and Kirkland,T.
Generation of ESTs from Coccidioides immitis spherule cDNA library

Oy	1	aaatgcgataagtaattgaaatcgaagatcatcgaatctcttgaacgcaca	60
Db	14	AAATTCGATTAAGTAATGTGAATTGCAGAAATTCGTAATCATCGAATCTTTGAAACGCACA	73
Oy	61	ttgcgcgccgcagtaattctgcgcggcatalgccttctcgaagcgatcatccaacctcaagcc	120
Db	74	TTTGGCCCTCTGTGTATTCGGGGGGCAATGCCGTTCGAGCGTCATTTGCAAACCTTTCAAG	133
Oy	121	cccgagtttgatglttcggggaatcgcgaagcccttgcgcgaagccggcccccgaatctagtg	180
Db	134	CACGCGCTTGTGTGTGGGCCAAACCTCCCGCGCTTGG--TGGACGGGCGCTGAATATGCAGTG	191
Oy	181	gcggc 184	
Db	192	gcgg 195	

	RESULT	2
	LOCUS	A1209736/c
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
TITLE	JOURNAL	COMMENT
		AI209736 213 bp mRNA linear EST 19-OCT-1998
		c7g08a1.f1 Aspergillus nidulans 24hr asexual developmental and
		vegetative cDNA lambda zap library Emericella nidulans cDNA clone
		c7g08a1_3' , mRNA sequence.
		AI209736
		AI209736.1 GI:3771678
		EST.
		Emericella nidulans.
		Emericella nidulans
		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
		Eurotiales; Trichocomaceae; Emericella.
		1 (bases 1 to 213)
		Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
		Prade,R. and Roe,B.
		An Aspergillus nidulans EST Database
		Unpublished (1998)
		Other-ESTs: c7g08a1.r1
		Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
		Department of Chemistry and Biochemistry
		Advanced Center for Genome Technology, University of Oklahoma
		620 Parrington Oval, Norman, OK 73019, USA
		Tel: 405 325 4912
		Fax: 405 325 7762
		Email: broeou.edu
		We anticipate the future release of the cDNA clones to the Fungal
		Genetics Stock Center
		Seq primer: M13-20.

FEATURES	SOURCE	Location/Qualifiers
		1. .213
		/organism="Emericella nidulans"
		/strain="FGSC A26"
		/db_xref="taxon:162425"
		/clone="c7g08a1"
		/clone_11b="Aspergillus nidulans 24hr asexual
		developmental and vegetative cDNA lambda zap library"
		/tissue.type="vegetative mycelia asexual structures"
		/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
		XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
		3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT		43 a 68 c 63 g 39 t
ORIGIN		

	Query Match	32.5%	Score 100.8;	DB 9;	Length 213;
	Best Local Similarity	74.5%;	Pred. No. 3.3e-20;		
	Matches 155; Conservative	0;	Mismatches 47;	Indels 6;	Gaps 2;
Oy	1 aaatcgataagatattgaattcgaattcaaatcatgatatctgaacttgaacgcaca	60			
Db	202 AACGCGCATAGTATGTGATTTCACAAATTCATGTGAATCTTCGAGCTTTGAACGCACA	143			
OY	61 ttgcgccggccagatattctgcgcggcacgtgccttgcttcgagcgtcaattccaacctcaagcc	120			

Db 142 TTGGGCCCCCGGCATTCCGGGGGGGCAATGCCGTGCAGAGGTCTATTCTGTCCCTCAAG-- 83

Oy 121 CCGGATGTTGTTGTTGGATCTCGCAAGCCTTCGCGCAAGCGGCCGGAATCTAGTg 18

Db 84 CCGCGCTTGTGCTATTGGGTCGTGCTCCCGCCCGGGG-----GACGGGCCCAAAAGCGACG 29

Oy 181 ggggtctgctgcagcttccattcgcta 208

Db 28 GCGGACCGCTGTCCGGGTCTCCGAGGCTA 1

RESULT	3
LOCUS	AI1213025/c
DEFINITION	AI1213025 318 bp mRNA linear EST 19-OCT-1998
ACCESSION	Y6101a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone Y6101a1.3', mRNA sequence.
VERSION	AI1213025
KEYWORDS	AI1213025.1 GI:3774967
SOURCE	EST.
ORGANISM	Emericella nidulans.
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eutroliales; Trichocomaceae; Emericella.
AUTHORS	1 (bases 1 to 318) Kupfer,D., Gray,J., Hausner,J., Lal,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE	An Aspergillus nidulans EST database
JOURNAL	unpublished (1998)
COMMENT	Other ESTs: Y6101a1.r1 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broeou.edu We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center Seq primer: M13-20 High quality sequence stop: 265.

FEATURES	SOURCE
Location/Qualifiers	
1. .318	
/organism="Emericella nidulans"	
/strain="FGSC A26"	
/db_xref="taxon:162425"	
/clone="y6f01a1"	
/clone_1lb="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"	
/tissue-type="vegetative mycelia, asexual structures"	
/note="Vector: plusscript SK; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of plusscript 3' end of cDNA cloned into XhoI site of plusscript"	
69 a 93 c 88 g 68 t	

Query Match	32.5%;	Score 100.8;	DB 9;	Length 318;
Best Local Similarity	74.5%;	Pred. No. 4e-20;		
Matches 153;	Conservative 0;	Mismatches 47;	Indels 6;	Gaps 2;
QY 1	aaatcgataaagtatgtgaattgcaaaatcagtaatcatcagaatcttggaaagcaca	60		
Db 204	AATGCGATAGTATGATGATTCAGATTCAGTCAATCTTGGAAACGCACA	145		
QY 61	tttgcgccccgagtaattcttgcgggcalgcctgttcttagcgtaattcaaccctcaagcc	120		
Db 144	TTTGCGCCCCCGCATTCGCGGGGGCATGCTCTTCGCGAGCTCATGTGCTCCCTCAAG--	85		
QY 121	cccgagtttggtttggggagacgcaagccctttgcgcaagccgcccccggaattcagtg	180		
Db 86	CCCGCGCTTGTGTGTGGTGCTGCTCCCCCGGGG---GACGGGGCCGAAAGCGACGCG	31		

oy	181	ggcgltcgcgcgcagcatccttcagcga	208
Db	30	CGCGCACCGTCTCGGTCTCGACGGA	3
RESULT	4		
CNS07820		846 bp	DNA
LOCUS			linear
DEFINITION			GSS 08-JUL-2001
			77 end of clone BB0AA025B03 of library BB0A from strain CBS 4732
ACCESSION			AL434652
VERSION			AL434652.1
KEYWORDS			GI:12218066
SOURCE			GSS.
ORGANISM			Pichia angusta.
REFERENCE			Pichia angusta.
AUTHORS			Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes: Saccharomycetales: Saccharomycetaceae: Pichia.
TITLE			1 (bases 1 to 846)
			Blandin,G., Florente,B., Malpertuy,A., Mincker,P., Attiguenave,F. and Dujon,B.
			Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta
JOURNAL			FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE			20584723
REFERENCE			2 (bases 1 to 846)
AUTHORS			Souciet,J.L., Aigle,M., Attiguenave,F., Blandin,G., Bojotin-Pukhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durres,P., Lepingle,A., Florente,B., Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toiffan-Nloche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
TITLE			Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL			FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE			20584711
REFERENCE			3 (bases 1 to 846)
AUTHORS			Genoscope.
TITLE			Direct Submission
JOURNAL			submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT			This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES			Location/Qualifiers
source			1..846
			/organism="Pichia angusta"
			/strain="CBS 4732"
			/db_xref="taxon:4905"
			/clone="BB0AA025B03"
			/clone_lib="BB0A"
			/note="end : 77"
			<1..>846
			/note="Part of rDNA repeats contains 35S rDNA"
			/evidence="not experimental"
BASE COUNT			224 a 165 c 188 g 267 t 2 others
ORIGIN			
Query Match			31.5%: Score 97.6; DB 12; Length 846;
Best Local Similarity			85.7%: Pred. No.5-8e-19;
Matches 120: conservative			0; Mismatches 19; Indels 1; Gaps 1;
oy	1	aagcgacgaagtaatgtgaattgcacaaatcagctgaatcgcgaatcttgaacgcaca	60

Oy	61	tttcgcccgcagatattcttgcggcgatcgtctgttcgaaggcatccaccccaagcc	120
Db	522	TTTTGGCCCTCGTGATTCGACAGGCGCATCCTTTTGGAGCGCTATTTC-CCTGTCAACC	580
Oy	121	cgcggatttgcttgcggaga	140
Db	581		600
Db	581	CTCGGCTTGGATGGGCA	600
RESULT	5		
CNS079EG			
LOCUS			
DEFINITION	T7 end of clone BB0AA028D03 of library BB0AA from strain CBS 4732		
ACCESSION	AL435182		
VERSION	AL435182.1		
KEYWORDS	GSS.		
SOURCE	Pichia angusta.		
ORGANISM	Pichia angusta.		
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
AUTHORS	Saccharomycetales; Saccharomycetaceae; Pichia.		
TITLE	1 (bases 1 to 893)		
JOURNAL	Blandin,G., Florente,B., Malpertuy,A., Wincker,P., Artiguenave,F.		
MEDLINE	and Dujon,B.		
REFERENCE	Genomic exploration of the hemiascomycetous yeasts: 13. Pichia		
AUTHORS	angusta		
TITLE	FEMS Lett. 487 (1), 76-81 (2000)		
JOURNAL	20584723		
MEDLINE	2 (bases 1 to 893)		
REFERENCE	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,		
AUTHORS	Bojotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,		
TITLE	de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B.,		
JOURNAL	Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,		
MEDLINE	Saurin,W., Tekala,P., Toffano-Nicchoe,C., Wesolowski-Louvel,M.,		
REFERENCE	Wincker,P. and Weissenbach,J.		
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 1. A set of		
TITLE	yeast species for molecular evolution studies		
JOURNAL	FEMS Lett. 487 (1), 3-12 (2000)		
MEDLINE	20584711		
REFERENCE	3 (bases 1 to 893)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,		
MEDLINE	2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :		
REFERENCE	seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
AUTHORS	This GSS is part of a random genomic sequencing program of thirteen		
TITLE	yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces		
JOURNAL	exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,		
MEDLINE	Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces		
REFERENCE	lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia		
AUTHORS	angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,		
TITLE	Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to		
JOURNAL	5 kb were prepared and both extremities were sequenced. See		
MEDLINE	keywords for description of this sequence and for the sequence of		
REFERENCE	the other extremity of this insert.		
AUTHORS	Location/Qualifiers		
TITLE	1..893		
JOURNAL	/organism="Pichia angusta"		
MEDLINE	/strain="CBS 4732"		
REFERENCE	/db_xref="taxon:4905"		
AUTHORS	/clone="BB0AA028D03"		
TITLE	/clone_1id="BB0AA"		
JOURNAL	/not_end = "T7"		
MEDLINE	<1..>893		
REFERENCE	/note="Part of rDNA repeats		
AUTHORS	contains 35S rDNA"		
TITLE	/evidence=not_experimental		
JOURNAL	BASE COUNT 244 a 160 c 226 g 261 t 2 others		
MEDLINE	ORIGIN		

TITLE
JOURNAL
MEDLINE
REFERENCE

JOURNAL
AUTHORS
TITLE
JOURNAL

COMMENT

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
20584711
3 (bases 1 to 981)

DIRECT SUBMISSION
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic Inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Location/Qualifiers
1..981

FEATURES
source

misc-feature

BASE COUNT
ORIGIN

Query Match
Best Local Similarity
Matches 119; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

Y 1 aaatcgataaagaatcgaattgcgaataaatgaagaaatcaatcgaattctttgaaacaca 60
Db 791 AAATCGAATAGCTATGTAATGGAAATTTCGTGCAATCATGAATTTTGAACGCACA 732

Y 61 ttggccgccgcagatattctgcgcggcatgctgttcgtagcgatcattcaacctcaagcc 120
Db 731 TTGCCCCCTCTGCTGTAATTCACAGGCGATGCCGTGTGAGCGCATYTTC-CCCTCAAACC 673

Y 121 cccggagtttgatgttgtgggga 140
Db 672 CTCGGCGTTTGCTGATGGCCA 653

RESULT 12
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

A2927454 515 bp DNA linear GSS 01-APR-2001
476.dlt2ba06.sl Saccharomyces castellii NRRL Y-12630 Saccharomyces
castellii genomic clone 476.dlt2ba06.sl, DNA sequence.
A2927454
A2927454.1 GI:13498358
GSS.
Saccharomyces castellii.
Saccharomyces castellii.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE
AUTHORS
TITLE

Cliffen,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Gish
.M.R., Waterston,R.H. and Johnston,M.
Surveying saccharomyces genomes to identify functional elements by
comparative DNA sequence analysis
Unpublished (2001)
Contact: Johnston M
Department of Genetics

```

Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mjenetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
1. .515
/organism="Saccharomyces castellii"
/strain="NRRL Y-12630 (CBS 4309)"
/db_xref="taxon:27288"
/clone="476.d1s1e02.s1"
/clone.lib="Saccharomyces castellii NRRL Y-12630"
/note="Random genomic sequence"

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ORIGIN

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Best Local Similarity 81.2%; Pred. No. 1,1e-18;
Matches 112; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY      1 aatgcgataagtaatgtaattgcataaattcaagtaatcagaatcttgaacgcaca 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      353 AATGCGAATACGTAATGCAATTCGCAATTCGTAATCATGCAATCTTGAACGCACA 294

QY      61 ttgcgcgcgcacgaattctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      293 TTGCGGCCCTTGTAATCCAGGGGCGCATCCCTGTTGACCGTCATTTCTTCAAAAGAA 234

QY      121 cccgcggttgctgctgtgg 138
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      233 CTTCTCTTGTGTAGTGCAG 216

RESULT 13
A2926778/c
LOCUS      A2926778
DEFINITION      A2926778 522 bp DNA linear GSS 01-APR-2001
ACCESSION      A2926778
VERSION      A2926778
KEYWORDS      A2926778.1 GI:13497680
SOURCE      GSS.
ORGANISM      Saccharomyces castellii.
              Saccharomyces castellii
              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
              Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE      1 (bases 1 to 522)
AUTHORS      Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Gish
              W.R., Waterston,R.H. and Johnson,M.
              Surveying Saccharomyces genomes to identify functional elements by
              comparative DNA sequence analysis
              Unpublished (2001)
JOURNAL
COMMENT      Contact: Johnston M
              Department of Genetics
              Washington University Medical School
              Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
              Tel: 314 362 2735
              Fax: 314 362 7855
              Email: mjenetics.wustl.edu
              Class: random plasmid subclone.
              Location/Qualifiers
              1. .522
              /organism="Saccharomyces castellii"
              /strain="NRRL Y-12630 (CBS 4309)"
              /db_xref="taxon:27288"
              /clone="476.d1s1e02.s1"
              /clone.lib="Saccharomyces castellii NRRL Y-12630"
              /note="Random genomic sequence"

BASE COUNT      156 a      106 c      107 g      153 t
ORIGIN

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[illegible]

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ORIGIN	/evidence-not-experimental				
Query Match	31.0% Score 96.2; DB 12; Length 870;				
Best Local Similarity	80.1% Pred. NO. 1.6e-18;				
Matches 113;	Conservative 0; Mismatches 28; Indels 0; Gaps 0;				
QY	1 aaatgcatgaagtaatgtaattgcaaaatctcagtgaaatcagaaatcttgaacgcaca 60				
Db	575 AATGCGATACGTAATGTAATTCGAGATATCCGATCATCAATCTTGAACGCACA 634				
QY	61 ttgcgcgcgcgaatctcgcgcgcacgcgcgtttcagcagcattcattcaacccctcaagcc 120				
Db	635 TTGGCGCCCTGTGTAATTCAGGGGCGATCGCTTTTGAGCCTCATTTCTTCMAACAG 694				
QY	121 ccgcgggttggtgttggtggat 141				
Db	695 CAATGTTTGGTTGTGAGTGAT 715				

CNS06KGF	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CNS06KGF	1004 bp	DNA	GSS 17-JUN-2001	T3 end of clone AT0A005B03 of library AT0A from strain CBS 4311	of Saccharomyces servazzii, genomic survey sequence.	AL402853	GI:12162391
GSS.							
Saccharomyces servazzii.							
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;							
Saccharomycetales; Saccharomycetaceae; Saccharomyces.							
1 (bases 1 to 1004)							
Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,							
Artiguenave,F., Wincker,P. and Galliardin,C.							
Genomic exploration of the hemiascomycetous yeasts: 7.							
Saccharomyces servazzii							
FEBS Lett. 487 (1), 47-51 (2000)							
20584717							
2 (bases 1 to 1004)							
Soucie,J.L., Aigle,M., Artiguenave,F., Blandin,G.,							
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,							
de-Montigny,D., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,							
Malberuy,A., Neuveglise,C., Ozler,Kalogoropoulos,O., Potier,S.,							
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,							
Winker,P. and Weissenbach,J.							
Genomic exploration of the hemiascomycetous yeasts: 1. A set of							
yeast species for molecular evolution studies							
FEBS Lett. 487 (1), 3-12 (2000)							
20584711							
3 (bases 1 to 1004)							
Genoscope.							
Direct Submission							
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,							
2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :							
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)							
This GSS is part of a random genomic sequencing program of thirteen							
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces							
equisus, Saccharomyces servazzii, Zygosaccharomyces rouxii,							
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces							
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia							
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,							
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to							
5 kb were prepared and both extremities were sequenced. See							
keywords for description of this sequence and for the sequence of							
the other extremity of this insert.							
Location/Qualifiers							
1..1004							
/organism='Saccharomyces servazzii'							
/strain='CBS 4311'							
/db_xref='taxon:27293'							

RESULT 2
US-08-905-314A-24
Sequence 24, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..181
OTHER INFORMATION: /note="18S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note="18S 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note="5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 80.6%; Score 249.8; DB 1; Length 561;
Best Local Similarity 91.6%; Pred. No. 3.2e-72;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;
Oy 1 aaatgcataaagtaatgtgaatgcataatcagtcgaatccttgaacgcaca 60

DB 232 AAATGCATTAAGTAATGTAATGCAGAAATTCAGTGAATCATGCAATCTTGAACGCACA 291
Oy 61 ttgcgcccgcagatattcgtggcagtcgcttgcagcgtatcttaaccctcaagcc 120
DB 292 TTGCGCCCGCTGTAATTCGCCGGGCATGCTGTTGAGGCTCATTTCAACCTCAAGCC 351
Oy 121 cccggtttgtgttggaatcgcgaagcccttcgagc-aagccgagccgaatactagt 179
DB 352 CCGCGTTTGTTGTTGGGATGCGCTGCTTMYGCGGTCGCCGCCCGCAATACATT 411
Oy 180 ggcgctcgcgtcagcttcacattgcgtagtagtaaaaaaccctcgcaactgtaacggcg 239
DB 412 GCGCGTCTCGCTGCAGCTCATTCGAGTAGCTACACACTGGAACGCGCGC 471
Oy 240 cggcagcgcgttaaccctcaacttcgaatgtttgaccttcgatacggtaggaataacc 299
DB 472 CGGCGATGCCG-TAAACCCCACTTGAATGTTGACCTCGATCGAGTAGAATACCC 530
Oy 300 gctgaactaa 310
DB 531 GCTGAACCTAA 541

RESULT 3
US-08-652-127C-8
Sequence 8, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 583
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-8

Query Match 74.5%; Score 231; DB 1; Length 583;
Best Local Similarity 90.4%; Pred. No. 4.4e-66;
Matches 281; Conservative 0; Mismatches 25; Indels 5; Gaps 3;
Oy 1 aaatgcataaagtaatgtgaatgcataatcagtcgaatccttgaacgcaca 60
DB 257 AAATGCATTAAGTAATGTAATGCAGAAATTCAGTGAATCATGCAATCTTGAACGCACA 316

OY 61 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 120
|||||
Db 317 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 376
OY 121 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 180
|||||
Db 377 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 435
OY 181 ggggtctgctgcagcttcacatgtagtaagtaaaacccctcgcaactgtagcgcgagc 240
|||||
Db 436 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 492
OY 241 gggcaagccgttaaaccccgcaactctgaatg-tgaacttggatgaggttagaagatccc 299
|||||
Db 493 gggcaagccgttaaaccccgcaactctgaatg-tgaacttggatgaggttagaagatccc 552
OY 300 gctgaactaa 310
|||||
Db 553 gctgaactaa 563

RESULT 4
US-08-652-127C-7
Sequence 7, Application US/08652127C
Patent No. 5792611

GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-7

Query Match 72.6% Score 225.2; DB 1: Length 511;
Best Local Similarity 86.8%; Pred. No. 3.3e-64;
Matches 277; Conservative 0; Mismatches 30; Indels 5; Gaps 3;
OY 1 aaatgcgataagtaatgtaatgcaaaatcagtaacatcgaatccttgaagcgaca 60
|||||
Db 203 aaatgcgataagtaatgtaatgcaaaatcagtaacatcgaatccttgaagcgaca 262
OY 61 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 120
|||||
Db 263 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 322

OY 121 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 179
|||||
Db 323 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 382
OY 180 ggggtctgctgcagcttcacatgtagtaagtaaaacccctcgcaactgtagcgcgagc 239
|||||
Db 383 ggggtctgctgcagcttcacatgtagtaagtaaaacccctcgcaactgtagcgcgagc 439
OY 240 gggcaagccgttaaaccccgcaactctg-aatgttgcactcgatcgaatgtagaagatccc 298
|||||
Db 440 gggcaagccgttaaaccccgcaactctg-aatgttgcactcgatcgaatgtagaagatccc 499
OY 299 cgctgaactaa 310
|||||
Db 500 cgctgaactaa 511

RESULT 5
US-08-652-127C-6
Sequence 6, Application US/08652127C
Patent No. 5792611

GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 581
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-6

Query Match 72.3% Score 224.2; DB 1: Length 581;
Best Local Similarity 88.5%; Pred. No. 7.1e-64;
Matches 276; Conservative 1; Mismatches 30; Indels 5; Gaps 3;
OY 1 aaatgcgataagtaatgtaatgcaaaatcagtaacatcgaatccttgaagcgaca 60
|||||
Db 253 aaatgcgataagtaatgtaatgcaaaatcagtaacatcgaatccttgaagcgaca 312
OY 61 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 120
|||||
Db 313 ttggccgcccagatattctggcgggcagtcgtctgttcgagcgctcaattcaccctcaagcc 372
OY 121 ccggggttgggttggttggaatggaacgagcccttgcggaagccggcccggaatctagt 179
|||||

Db 373 CCGGGCTTGTGTGGAGATCGCGTCCCGGGGGCCGCTCCCAATATAGT 432
Oy 180 ggcggctcgcgtgcagctccatcgtcgtagtaaaacccctgcgaactggtacgcgcg 239
Db 433 GCGGCTTCGCTGTAAGTCTTCTCTGCTAGTAGACACACTTGGC---ACTGGAANAACAGCG 489
Oy 240 cggccaagccgttaaaccccaactctctg-aatgttcgacctcgatcagtaggaataacc 298
Db 490 TGGCCACGCGGCTTAACCCCGCACTTGTGAAGGTTGACCTGCGATCAGTAGAATACC 549
Oy 299 cgcctgaacttaa 310
Db 550 CGCTGAACCTTA 561

RESULT 6
US-08-652-127C-5
; Sequence 5, Application US/08652127C

; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-5

Query Match 63.8%; Score 197.8; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 2,9e-55;
Matches 271; Conservative 0; Mismatches 37; Indels 11; Gaps 4;

Oy 1 aaatcgataaataatgcaaatcgaatgataatcgaatcttgaagaagca 60
Db 258 AAATCGATAAATGATGAAATGCAAAATTCAGTAATCATCGAATCTTGAACGCACA 317
Oy 61 ttgcgcccgcagtaattcggcgggcagtcgttcgagcgltcaatccaacctcaagcc 120
Db 318 TTGCGCCCGCGCATATCTGGCGGCGCATGCTGTCGAGCGTCAATTCACCCCTCAAGCA 377
Oy 121 cc-----cgggttcgttcgtgggagtcggcgaag-----cccttcgcggaagccgcgcgca 172
Db 378 CCTTCGGAGAGCTGTGGTGTGGGATCGGCAGGCGCTCCTCCGCGGCGCGCTCCCCCAA 437
Oy 173 atctagtcggttcgctgcagctcattcgtagtagtaaaacctgcgaactgtta 232

Db 438 ATCTAGTGGCGGTCTGCTACTTCTCTGCTAGTAATACA--CTTCGCTCTGAGT 495
Oy 233 cggcgggcgccgaagccgttaaaccccccaactctgaat-gttgacctcgatcagtag 291
Db 496 CTCGCTCGGCGCACGCGGTAAACCCCGCAACTTTTCTGTGACCTCGAATCAGTAG 555
Oy 292 gaataccgctgaacttaa 310
Db 556 GACTACCGCGCTGAACCTTA 574

RESULT 7
US-08-887-480-96
; Sequence 96, Application US/08887480

; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal pathogens Using the
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 581453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meligs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium poae
; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus
; IMMEDIATE SOURCE: sequence)
; CLONE: PCRFOAet427(1-2), PCRFOAet534(2-2), and
; FEATURE: PCRFOAet756(3-1)
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit
; FEATURE: rRNA gene"
; NAME/KEY: misc_feature
; LOCATION: 31..180
; OTHER INFORMATION: /note="ITS 1"
; NAME/KEY: misc_feature
; LOCATION: 181..337

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:
: OTHER INFORMATION: /note= "5.8S rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 338..489
:   OTHER INFORMATION: /note= "ITS 2"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 490..546
:   OTHER INFORMATION: /note= "5' end of large subunit"
:   OTHER INFORMATION: rRNA gene"
:
US-08-887-480-96

Query Match      60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 5.8e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

OY 1 aatgagataaataatgtaattgcaaaaatcagatgcatcgaattcttgaacgaca 60
    |||||||
DB 231 AATGCGATGAAGTAATGTAATGCGAATTCAGTCAATCGAATCTTTGAACGCACA 290

OY 61 ttgcgcccgcagatcttcgagcgccatcgttcgagcgatcattcaaccctcaagcc 120
    |||||||
DB 291 TTGCGCGCCGCGATATCTGGCGGCGATGCGTTCGAGCGTCATTTCAACCCCTCAAGCC 350

OY 121 cccgggttggtgttgaggatcggcaagcccttcggcgcaagccgcccgaattcagt 180
    |||||||
DB 351 C--ACCTTGCTGTGGG-----ATCTGTGCAAAACACAGTCCCAATTTGATTG 398

OY 181 ggggtctgcagcttcacatcgttcgtagtagtaaaacctcgcaacgtgtagcgggcg 240
    |||||||
DB 399 GCGGTACG-TCGAGCTTCCATAGCGTATATTACACATCGTATGTAATGTCGCG 457

OY 241 ggcgaagccgttaaaccccccaacttcgaatgttgacctcgatcgaagtaggaataccg 300
    |||||||
DB 458 GGCACGCGCGTTAA-CCCCAATTCTGAATGTTGACCTCGGATCAGTAGAATATCCCG 516

OY 301 ctgaactaa 310
    |||||||
DB 517 CTGAACCTTAA 526

RESULT 8
US-08-905-314A-22
: Sequence 22, Application US/08905314A
: Patent No. 5827695
: GENERAL INFORMATION:
:   APPLICANT: Beck, James J.
:   TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
:   TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
:   NUMBER OF SEQUENCES: 24
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: No. 5827695artis Corporation Patent Department
:     STREET: 3054 Cornwallis Road
:     CITY: Research Triangle Park
:     STATE: NC
:   COUNTRY: USA
:   ZIP: 20779-2257
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/905,314A
:     FILING DATE:
:     CLASSIFICATION: 435
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Meigs, J. Timothy
:     REGISTRATION NUMBER: 38,241
:     REFERENCE/DOCKET NUMBER: CGC 1944
:     TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (919) 541-8587
```

```

:
: TELEFAX: (919) 541-8689
:
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 546 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
:   ORGANISM: Fusarium poae
:   INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
:   INDIVIDUAL ISOLATE: sequence)
: IMMEDIATE SOURCE:
:   CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
:   CLONE: pCRFpoaeT756(3-1)
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 1..30
:   OTHER INFORMATION: /note= "3' end of small subunit"
:   OTHER INFORMATION: rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 31..180
:   OTHER INFORMATION: /note= "ITS 1"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 181..337
:   OTHER INFORMATION: /note= "5.8S rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 338..489
:   OTHER INFORMATION: /note= "ITS 2"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 490..546
:   OTHER INFORMATION: /note= "5' end of large subunit"
:   OTHER INFORMATION: rRNA gene"
:
US-08-905-314A-22

Query Match      60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 5.8e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

OY 1 aatgagataaataatgtaattgcaaaaatcagatgcatcgaattcttgaacgaca 60
    |||||||
DB 231 AATGCGATGAAGTAATGTAATGCGAATTCAGTCAATCGAATCTTTGAACGCACA 290

OY 61 ttgcgcccgcagatcttcgagcgccatcgttcgagcgatcattcaaccctcaagcc 120
    |||||||
DB 291 TTGCGCGCCGCGATATCTGGCGGCGATGCGTTCGAGCGTCATTTCAACCCCTCAAGCC 350

OY 121 cccgggttggtgttgaggatcggcaagcccttcggcgcaagccgcccgaattcagt 180
    |||||||
DB 351 C--AGCTTGGTGTGGG-----ATCTGTGCAAAACACAGTCCCAATTTGATTG 398

OY 181 ggggtctgcagcttcacatcgttcgtagtagtaaaacctcgcaacgtgtagcgggcg 240
    |||||||
DB 399 GCGGTACG-TCGAGCTTCCATAGCGTATATTACACATCGTATGTAATGTCGCG 457

OY 241 ggcgaagccgttaaaccccccaacttcgaatgttgacctcgatcgaagtaggaataccg 300
    |||||||
DB 458 GGCACGCGCGTTAA-CCCCAATTCTGAATGTTGACCTCGGATCAGTAGAATATCCCG 516

OY 301 ctgaactaa 310
    |||||||
DB 517 CTGAACCTTAA 526

RESULT 9
US-08-887-480-82
: Sequence 82, Application US/08887480
: Patent No. 5814453
```

GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 96
TITLE OF INVENTION: Polymerase Chain Reaction
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 581453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 319..472
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-887-480-82

Query Match 60.2%; Score 186.6; DB 1; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.2e-51;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;
1 aaatcgataagtaatgtaattgcagaaattcgtaacatcgaactcttgaacgaca 60
|||||

Db 212 AAATGCATAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGACA 271
Qy 61 ttgcgcccagcatatctcgtgagcgtgagcgtcattcaaccctcaagcc 120
|||||
Db 272 TTGGGCCCCGACATATCTGGCGGCGCATGCTGTTCAGAGCTCATTTCAACCTCAAGCC 331
Qy 121 cccgagtttggttggtgagatcgcaagccctgcgcaagccgcccgaatctagtg 180
|||||
Db 332 C---AGCTTGCTGTGGG-----AGCTGCAGTCTGCTGCCTCCCAAAATACATTC 380
Qy 181 gcgctcgtcgcaggtctcattgctgtagtaaacctcgcgaactgtagcgagcg 240
|||||
Db 381 GCGGTACGCTGACGCTTCCATAGCTAGTAATTTACATATCTTACTGGTAATCGTCG 440
Qy 241 ggcgaagccgttaaaccccaactctgaattgtaccctcgatcagtaggaataccg 300
|||||
Db 441 GGCYACGCCGTTAA-CCCAACTTGTGAATGTGACTCGGATCGAGTGAATATACCG 499
Qy 301 ctgaa 305
|||||
Db 500 CTGAA 504

RESULT 10
US-08-905-314A-19
Sequence 19, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature


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LOCATION: 179..335
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 336..488
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 489..545
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-21
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Query Match

59.1%; Score 183.2; DB 1; Length 545;

Best Local Similarity 83.5%; Pred. No. 1.6e-50;

Matches 259; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

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Db 289 TTGCGCCCGCGCAGATTCTGCGCGCATGCGCTTTCGACGCTATTTC AACCTCAAGCC 348
QY 121 cccgggttgggtctcgggagtcgcaagcccttcgcaagccgccccgaaatctagtg 180
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QY 181 gcggttcgctgagcttcgattgctgtagtaaaacctcgcaactgtaagcgcg 240
Db 398 GCGGTACG-TCGAGCTTCATAGCGTGAATTTACACATCGTTACTGTATCGTGC 456
QY 241 gccaagccgcltaaaccccaacttcgaatgtlgaacctgagctcgatcagtaggaataccg 300
Db 457 GGCACGCGCCTTAA-CCCAACTTCTGAATGTTGACCTCGATCAGTAGGAATACCCG 515
QY 301 ctgaacttaa 310
Db 516 CTGAACCTAA 525
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Search completed: August 21, 2002, 22:12:26
Job time: 3699 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:32 ; Search time 8184.59 Seconds

(without alignments)
47.581 Million cell updates/sec

Title: US-10-046-955-50

Sequence: 1 cgtcaatcgcgtccctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	18	100.0	382	US-09-241-427-3	Sequence 3, Appl
3	16.4	91.1	620	US-09-580-797-11	Sequence 11, Appl
4	15.4	85.6	25	US-09-954-427-166475	Sequence 166475,
5	15.4	85.6	25	US-60-233-166-166475	Sequence 166475,
6	15.4	85.6	6936	US-60-161-932-210	Sequence 210, App
7	15.4	85.6	6938	US-09-528-237A-186	Sequence 186, App
8	15.4	85.6	26475	US-60-161-932-109	Sequence 109, App
9	15.4	85.6	36240	US-09-528-237A-1558	Sequence 1558, Ap
10	15.4	85.6	41444	US-09-620-392-61180	Sequence 58840, A
11	15.4	85.6	41444	US-09-620-392-61180	Sequence 61180, A
12	15.4	85.6	41444	US-09-702-134-26530	Sequence 26530, A
13	15.4	85.6	41444	US-09-815-264-65941	Sequence 65941, A
14	15	83.3	128	PCT-US02-03987-996	Sequence 996, App
15	15	83.3	128	US-09-815-242-996	Sequence 996, App
16	15	83.3	128	US-09-815-242-996	Sequence 996, App
17	15	83.3	250	PCT-US02-03987-555	Sequence 555, App
18	15	83.3	250	US-09-815-242-555	Sequence 555, App
19	15	83.3	250	US-10-072-851-555	Sequence 555, App
20	15	83.3	250	US-09-815-242-555	Sequence 555, App
21	15	83.3	250	US-09-815-242-555	Sequence 555, App
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32 14.8 82.2 432 27 US-09-684-016-148514 Sequence 148514,
33 14.8 82.2 438 18 US-09-440-687-17246 Sequence 17246, A
34 14.8 82.2 438 25 US-09-654-617-69363 Sequence 69363, A
35 14.8 82.2 438 27 US-09-684-016-69363 Sequence 69363, A
36 14.8 82.2 438 53 US-60-144-084-13220 Sequence 1320, Ap
37 14.8 82.2 460 16 US-09-270-849B-32774 Sequence 32774, A
38 14.8 82.2 463 22 US-09-572-409-35481 Sequence 35481, A
39 14.8 82.2 468 16 US-09-270-849B-53297 Sequence 53297, A
40 14.8 82.2 481 17 US-09-304-517A-228553 Sequence 228553,
41 14.8 82.2 481 17 US-09-371-146A-228553 Sequence 228553,
42 14.8 82.2 481 36 US-09-985-678-228553 Sequence 228553,
43 14.8 82.2 481 51 US-60-125-817-7043 Sequence 7043, Ap
44 14.8 82.2 482 18 US-09-404-520-17444 Sequence 17444, A
45 14.8 82.2 650 1 PCT-US00-32639-103 Sequence 103, App
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ALIGNMENTS

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RESULT 1
US-09-423-233-50
; Sequence 50, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-423-233-50
```

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Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 cgttaattcgcttcctc 18
Db 1 cgttaattcgcttcctc 18
```

```
RESULT 2
US-09-241-427-3
; Sequence 3, Application US/09241427
; GENERAL INFORMATION:
; APPLICANT: Yechezkel Kashi et al.
; TITLE OF INVENTION: NUCLEIC ACID-BASED ASSAY AND KIT FOR THE
; TITLE OF INVENTION: DETECTION OF ALTERNARIA CONTAMINATION IN
; TITLE OF INVENTION: FOOD PRODUCTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2.
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,427
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/57
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-241-427-3
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Query Match 100.0%; Score 18; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 cgttaattcgcttcctc 18
Db 287 cgttaattcgcttcctc 304
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RESULT 3
US-09-580-797-11
; Sequence 11, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-580-797-11
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Query Match 91.1%; Score 16.4; DB 22; Length 620;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 cgttaattcgcttcctc 18
Db 478 cgttaattcgcttcctc 495
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```
RESULT 4
US-09-954-427-166475
; Sequence 166475, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mitterman
; APPLICANT: Altmietrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925863
US-09-954-427-166475
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Query Match      85.6%; Score 15.4; DB 35; Length 25;
Best Local Similarity 94.1%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      2 gctaatcgcgtctcct 18
        ||||||||| |||||||
Db      9 gctaatcggggtccctc 25
```

```
RESULT      5
US-60-233-166-166475
; Sequence 166475, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925863
US-60-233-166-166475
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```
Query Match      85.6%; Score 15.4; DB 62; Length 25;
Best Local Similarity 94.1%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy      2 gctaatcgcgtctcct 18
        ||||||||| |||||||
Db      9 gctaatcggggtccctc 25
```

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RESULT      6
US-60-161-932-210/C
; Sequence 210, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 6936
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-210
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Query Match      85.6%; Score 15.4; DB 55; Length 6936;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Oy      1 cgttaatcgcgtctcct 17
        ||| ||||||||| |||
Db      5984 CGTTCATTCGCGTTCTCT 5968
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```
RESULT      7
US-09-528-237A-186
; Sequence 186, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 6938
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-186
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Query Match      85.6%; Score 15.4; DB 19; Length 6938;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 cgttaatcgcgtctcct 17
        ||| ||||||||| |||
Db      954 cgttaatcgcgtctcct 970
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```
RESULT      8
US-60-161-932-109/C
; Sequence 109, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 26474
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-109
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Query Match      85.6%; Score 15.4; DB 55; Length 26474;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Oy      1 cgttaatcgcgtctcct 17
        ||||||||| |||
Db      1502 CGTTCATTCGCGTTCTCT 1486
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RESULT      9
US-09-528-237A-1558/C
; Sequence 1558, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
```

```
;; CURRENT APPLICATION NUMBER: US/09/528.237A
;; CURRENT FILING DATE: 2000-03-17
;; NUMBER OF SEQ ID NOS: 2926
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1558
;; LENGTH: 26475
;; TYPE: DNA
;; ORGANISM: Drosophila
US-09-528-237A-1558
```

```
Query Match      85.6%; Score 15.4; DB 19; Length 26475;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 gtaattcgcgttcctc 17
          |||||
Db      1503 CGTTAATTCGCTTCTCCT 1487
```

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RESULT 10
US-09-620-392-58840/C
; Sequence 58840, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 58840
; LENGTH: 36240
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-58840
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Query Match      85.6%; Score 15.4; DB 24; Length 36240;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          |||||
Db      14875 GTTAATTCACGCTTCCTC 14859
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```
RESULT 11
US-09-620-392-61180
; Sequence 61180, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 61180
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-61180
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Query Match      85.6%; Score 15.4; DB 24; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY      2 gtaattcgcgttcctc 18
          |||||
Db      20643 gtaattcgcgttcctc 20659
```

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RESULT 12
US-09-702-134-26530
; Sequence 26530, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 26530
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-26530
```

```
Query Match      85.6%; Score 15.4; DB 28; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          |||||
Db      20643 gtaattcgcgttcctc 20659
```

```
RESULT 13
US-09-815-264-65941
; Sequence 65941, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 65941
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-65941
```

```
Query Match      85.6%; Score 15.4; DB 31; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          |||||
Db      20643 gtaattcgcgttcctc 20659
```

RESULT 14
PCT-US02-03987-996/c
; Sequence 996, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for identifying the target of a compound which inhibits c
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
PCT-US02-03987-996

Query Match 83.3%; Score 15; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcggttc 16
|||||
DB 118 GTTAATTCGCGTTCC 104

RESULT 15
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996

Query Match 83.3%; Score 15; DB 31; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcggttc 16
|||||
DB 118 GTTAATTCGCGTTCC 104

Search completed: August 22, 2002, 00:39:40
Job time: 13065 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:53 ; Search time 663.62 Seconds
(without alignments)
72.981 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgtctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 172111 seqs, 1345317543 residues

3442222

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents, NA, New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-046-955-50	Sequence 50, Appl
2	14.4	80.0	25	US-09-956-604-95112	Sequence 95112, A
3	14.4	80.0	25	US-09-956-604-95113	Sequence 95113, A
4	14.4	80.0	26	US-09-975-254-9537	Sequence 9537, Ap
5	14.4	80.0	270	US-09-975-254-21902	Sequence 21902, A
6	14.4	80.0	651	US-10-027-632-266929	Sequence 266929, A
7	14.4	80.0	914	US-09-975-254-35000	Sequence 35000, A
8	14.4	77.8	2569	US-06-360-039-36500	Sequence 36500, A
9	13.8	76.7	251	US-09-975-254-30190	Sequence 30190, A
10	13.8	76.7	255	US-09-975-254-17320	Sequence 17320, A
11	13.8	76.7	255	US-09-975-254-17834	Sequence 17834, A
12	13.8	76.7	263	US-09-975-254-7020	Sequence 7020, Ap
13	13.8	76.7	366	US-10-098-754-13158	Sequence 13158, A
14	13.8	76.7	563	US-10-027-632-61031	Sequence 61031, A
15	13.8	76.7	563	US-10-027-632-309725	Sequence 309725, A
16	13.8	76.7	663	US-10-027-632-230673	Sequence 230673, A
17	13.8	76.7	774	US-06-360-039-29878	Sequence 29878, A
18	13.8	76.7	905	US-10-098-754-18470	Sequence 18470, A
19	13.8	76.7	1163	US-06-360-039-30593	Sequence 30593, A
20	13.8	76.7	1248	US-09-540-2098-168	Sequence 168, App
21	13.8	76.7	3854	US-10-205-219-186	Sequence 186, App
22	13.8	76.7	6642	US-09-545-199F-80	Sequence 80, Appl
23	13.8	76.7	9423	US-10-101-840-6	Sequence 6, Appl
24	13.8	76.7	9704	US-10-109-860-3	Sequence 3, Appl
25	13.8	76.7	12666	US-10-158-844-137	Sequence 137, App

26	13.8	76.7	13046	US-10-125-540-595	Sequence 595, App
27	13.8	76.7	24607	US-10-027-632-76188	Sequence 76188, A
28	13.8	76.7	49650	US-10-053-853A-410	Sequence 410, App
29	13.8	76.7	49795	US-10-114-170-60	Sequence 60, Appl
30	13.8	76.7	185548	PCT-US02-19457-62	Sequence 62, Appl
31	13.8	76.7	185548	US-10-175-523-62	Sequence 17011, A
32	13.4	74.4	349	US-09-721-544-17011	Sequence 14313, A
33	13.4	74.4	435	US-09-785-276A-14313	Sequence 35427, A
34	13.4	74.4	455	US-09-785-276A-44259	Sequence 44259, A
35	13.4	74.4	455	US-09-785-276A-44259	Sequence 5144, Ap
36	13.4	74.4	457	US-09-785-276A-5144	Sequence 22342, A
37	13.4	74.4	466	US-09-918-995-22342	Sequence 54492, A
38	13.4	74.4	608	US-09-785-276A-54492	Sequence 1236, Ap
39	13.4	74.4	665	US-06-377-240-1236	Sequence 23251, A
40	13.4	74.4	686	US-09-785-276A-23251	Sequence 29125, A
41	13.4	74.4	686	US-09-785-276A-29125	Sequence 34822, A
42	13.4	74.4	842	US-06-360-039-34823	Sequence 8724, Ap
43	13.4	74.4	902	US-10-198-846-8724	Sequence 5152, Ap
44	13.4	74.4	1089	US-09-540-2098-5152	Sequence 261, App
45	13.4	74.4	1196	US-10-137-337-261	

ALIGNMENTS

RESULT 1
US-10-046-955-50
Sequence 50, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium oxysporum
US-10-046-955-50
Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 cgttaatcgcgtctc 18
OY |||||
Db 1 cgttaatcgcgtctc 18
RESULT 2
US-09-956-604-95112/C
Sequence 95112, Application US/09956604
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604

```
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95112
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-95112
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ttaattcgcttcctc 18
        |||||||
Db      16 TTAAATCGCGTTCCTC 1
```

```
RESULT      3
US-09-956-604-95113/C
; Sequence 95113, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-95113
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ttaattcgcttcctc 18
        |||||||
Db      20 TTAAATCGCGTTCCTC 5
```

```
RESULT      4
US-09-975-254-9537
; Sequence 9537, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 9537
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700756034H1
US-09-975-254-9537
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 26;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ttaattcgcttcctc 18
        |||||||
Db      7 ttgattcgcttcctc 22
```

```
RESULT      5
US-09-975-254-21902
; Sequence 21902, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 21902
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700960259H1
US-09-975-254-21902
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 270;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ttaattcgcttcctc 18
        |||||||
Db      43 ttgattcgcttcctc 58
```

```
RESULT      6
US-10-027-632-266929/C
; Sequence 266929, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266929
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-266929
```

Query Match 80.0%; Score 14.4; DB 7; Length 651;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gtaattcgcttct 17
||||| |||||||
DB 312 GTTAATCGCCTTCT 297

RESULT 7

US-60-360-039-35000
; Sequence 35000, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35000
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Methanosarcina mazei
US-60-360-039-35000

Query Match 80.0%; Score 14.4; DB 8; Length 914;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gtaattcgcttct 17
||||| |||||||
DB 611 gtaattcgcttct 626

RESULT 8

US-60-360-039-36500
; Sequence 36500, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36500
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-360-039-36500

Query Match 77.8%; Score 14; DB 8; Length 2569;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 aatcgcttctc 18
||||| |||||||
DB 599 aatcgcttctc 612

RESULT 9

US-09-975-254-30190
; Sequence 30190, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 30190
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700901009H1
US-09-975-254-30190

Query Match 76.7%; Score 13.8; DB 5; Length 251;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaattcgcttct 17
||||| |||||||
DB 52 cgttaattcgcttct 68

RESULT 10

US-09-975-254-17320
; Sequence 17320, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17320
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700954206H1
US-09-975-254-17320

Query Match 76.7%; Score 13.8; DB 5; Length 255;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaattcgcttct 17
||||| |||||||
DB 170 cgttaattcgcttct 186

RESULT 11

US-09-975-254-17834
; Sequence 17834, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B

```
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17834
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700954789H1
US-09-975-254-17834
```

```
Query Match          76.7%; Score 13.8; DB 5; Length 255;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 cgttaatcgcgttcc 17
Db 169 cgttaatcattcttcc 185
```

```
RESULT 12
US-09-975-254-7020
; Sequence 7020, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 7020
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700752705H1
US-09-975-254-7020
```

```
Query Match          76.7%; Score 13.8; DB 5; Length 263;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 cgttaatcgcgttcc 17
Db 174 cgttaatcattcttcc 190
```

```
RESULT 13
US-10-098-754-13158
; Sequence 13158, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; APPLICANT: Ramachandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: ATX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 21107
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13158
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; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(366)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-13158
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Query Match          76.7%; Score 13.8; DB 6; Length 366;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 2 gtaattcgcgttcc 18
Db 294 gtaattcattcttcc 310
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RESULT 14
US-10-027-632-61031/c
; Sequence 61031, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61031
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-61031
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Query Match          76.7%; Score 13.8; DB 7; Length 563;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 2 gtaattcgcgttcc 18
Db 162 gtttaattcgcgttcttcc 146
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RESULT 15
US-10-027-632-309725/c
; Sequence 309725, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 309725
: LENGTH: 563
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-309725

Query Match 76.7%; Score 13.8; DB 7; Length 563;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 2 gtaatcgcgttcctc 18
||||| ||||| |||
Db 162 CTTAAGTCGCGCTTCTTC 146

Search completed: August 22, 2002, 00:50:57
Job time: 11897 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:51 ; Search time 2238.68 Seconds

(Without alignments)
196.302 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaacacctgcgaactgagaga 21

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_in:*
32: em_hlg_other:*
33: em_higo_in:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

Result	No.	Query	Match	Length	DB	ID	Description
1	21	100.0	319	8	AF117921		AF117921 Nectria h
2	21	100.0	471	8	AF161222		AF161222 Fusarium
3	21	100.0	471	8	AY043472		AY043472 Haematone
4	21	100.0	471	8	AY043473		AY043473 Haematone
5	21	100.0	471	8	AY043478		AY043478 Haematone
6	21	100.0	477	8	FS038558		U38558 Fusarium so
7	21	100.0	478	8	AF132801		AF132801 Nectria h
8	21	100.0	478	8	AF150459		AF150459 Nectria h
9	21	100.0	478	8	AF150460		AF150460 Nectria h
10	21	100.0	478	8	AF150461		AF150461 Nectria h
11	21	100.0	478	8	AF150462		AF150462 Nectria h
12	21	100.0	478	8	AF150463		AF150463 Nectria h
13	21	100.0	478	8	AF150464		AF150464 Nectria h
14	21	100.0	478	8	AF150465		AF150465 Nectria h
15	21	100.0	479	8	AF150469		AF150469 Nectria h
16	21	100.0	479	8	AF150470		AF150470 Nectria h
17	21	100.0	479	8	AF150475		AF150475 Nectria h
18	21	100.0	480	8	AF150466		AF150466 Nectria h
19	21	100.0	480	8	AF150467		AF150467 Nectria h
20	21	100.0	480	8	AF150477		AF150477 Nectria h
21	21	100.0	480	8	AF150478		AF150478 Nectria h
22	21	100.0	480	8	AF150479		AF150479 Nectria h
23	21	100.0	480	8	AF150480		AF150480 Nectria h
24	21	100.0	480	8	AF440567		AF440567 Nectria h
25	21	100.0	483	8	FS038557		U38557 Fusarium so
26	21	100.0	483	8	AY043477		AY043477 Haematone
27	21	100.0	505	8	AY043470		AY043470 Haematone
28	21	100.0	509	8	AF165874		AF165874 Nectria h
29	21	100.0	544	8	NEXTS		L36627 Neocosmospo
30	21	100.0	546	8	AF178413		AF178413 Neocosmos
31	21	100.0	547	8	AF178412		AF178412 Neocosmos
32	21	100.0	547	8	NECTISA		L36619 Nectria hae
33	21	100.0	548	8	AF178397		AF178397 Fusarium
34	21	100.0	548	8	AF178402		AF178402 Fusarium
35	21	100.0	549	8	AF178398		AF178398 Nectria 1
36	21	100.0	550	8	AF178394		AF178394 Nectria 1
37	21	100.0	550	8	AF178401		AF178401 Nectria h
38	21	100.0	550	8	AF178407		AF178407 Fusarium
39	21	100.0	550	8	AF178408		AF178408 Fusarium
40	21	100.0	550	8	AF178422		AF178422 Fusarium
41	21	100.0	569	8	AF129104		AF129104 Nectria h
42	20	95.2	471	8	AY043469		AY043469 Haematone
43	20	95.2	471	8	AY043476		AY043476 Haematone
44	20	95.2	475	8	AY043475		AY043475 Haematone
45	19.4	92.4	477	8	AY043474		AY043474 Haematone

ALIGNMENTS

RESULT 1
AF117921
LOCUS AF117921 319 bp DNA linear PLN 17-JUN-2000
DEFINITION Nectria haematococca 5.8S ribosomal RNA gene, partial sequence;
Internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.

ACCESSION AF117921 GI:8570107
VERSION
KEYWORDS
SOURCE
ORGANISM
Nectria haematococca.
Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE
AUTHORS Choi,J.S., Westerman,J.M. and Morrison,C.J.
TITLE Rapid differentiation of filamentous fungi using species-specific
DNA probes
JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
2 (bases 1 to 319)

REFERENCE
AUTHORS Choi,J.S., Westerman,J.M. and Morrison,C.J.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

FEATURES

source Location/Qualifiers

1..319
/organism="Nectria haematococca"
/db_xref="taxon:140110"

rRNA
159
/product="5.8S ribosomal RNA"
160..272
/note="ITS2"
/product="Internal transcribed spacer 2"
273..>319
/product="28S ribosomal RNA"

BASE COUNT 77 a 96 c 84 g 62 t

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 222 CTAACACTCGCACTGAGAG 242

RESULT 2
AF161222 471 bp DNA linear PLN 09-FEB-2000
LOCUS
DEFINITION Fusarium solani internal transcribed spacer 1, partial sequence;
5.8S ribosomal RNA gene, complete sequence; internal transcribed
spacer 2, and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF161222
VERSION AF161222.1 GI:6941832
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Grunden, E., Chen, W., and Crane, J. L.
JOURNAL Fungi Colonizing Microsclerotia of Verticillium dahliae
REFERENCE 2 (bases 1 to 471)
AUTHORS Grunden, E., Chen, W., and Crane, J. L.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural
History Survey, IL Dept. Natural Resources, 607 E. Peabody Dr.,
Champaign, IL 61820, USA

FEATURES

source Location/Qualifiers

1..471
/organism="Nectria haematococca"
/db_xref="taxon:140110"

misc_RNA
117
/note="ITS1"
/product="Internal transcribed spacer 1"
118..276
/product="5.8S ribosomal RNA"
277..450
/note="ITS2"
/product="Internal transcribed spacer 2"
451..>471
/product="28S ribosomal RNA"

rRNA
451..>471
/product="Internal transcribed spacer 2"

BASE COUNT 121 a 133 c 117 g 100 t

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 390 CTAACACTCGCACTGAGAG 410

RESULT 3
AY043472/c 471 bp DNA linear PLN 05-SEP-2001
LOCUS
DEFINITION Haemonectria haematococca strain 35 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AY043472
VERSION AY043472.1 GI:15450333
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Miller, R.N.G. and Lopes, C.A.
JOURNAL rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil

FEATURES

source Location/Qualifiers

1..471
/organism="Nectria haematococca"
/strain="35"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani!"
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"

BASE COUNT 94 a 121 c 136 g 118 t 2 others

ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 59 CTAACACTCGCACTGAGAG 39

RESULT 4
AY043473/c 471 bp DNA linear PLN 05-SEP-2001
LOCUS
DEFINITION Haemonectria haematococca strain 39 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AY043473
VERSION AY043473.1 GI:15450334
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Miller, R.N.G. and Lopes, C.A.
JOURNAL rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil

FEATURES

source Location/Qualifiers

1..471

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/organism="Nectria haematococca"
/strain="39"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani1"
complement(1..471)
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"
BASE COUNT      92 a      118 c      142 g      118 t      1 others
ORIGIN

Query Match      100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactgaga 21
|||||
Db      60 CTACACCTCGCAACTGAGAGA 40

RESULT 5
AY043478/c      471 bp      DNA      linear      PLN 05-SEP-2001
LOCUS
DEFINITION      Haematococcia haematococca strain 83 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION      AY043478
VERSION      AY043478.1 GI:15450339
KEYWORDS
SOURCE      Nectria haematococca.
Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE      1 (bases 1 to 471)
AUTHORS      Miller,R.N.G. and Lopes,C.A.
TITLE      rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
JOURNAL      Unpublished
2 (bases 1 to 471)
AUTHORS      Miller,R.N.G. and Lopes,C.A.
TITLE      Direct Submission
JOURNAL      Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catoilica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil
FEATURES
source      location/Qualifiers
1..471
/organism="Nectria haematococca"
/strain="83"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani1"
complement(1..471)
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"
BASE COUNT      91 a      120 c      138 g      121 t      1 others
ORIGIN

Query Match      100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactgaga 21
|||||
Db      59 CTACACCTCGCAACTGAGAGA 39

RESULT 6
FSU38558      477 bp      DNA      linear      PLN 08-NOV-1995
LOCUS
DEFINITION      Fusarium solani 5.8S ribosomal RNA gene, complete sequence and
internal transcribed spacers 1 and 2.
ACCESSION      U38558
VERSION      U38558.1 GI:1054930
```

```
KEYWORDS      Fusarium solani.
SOURCE      Nectria haematococca
ORGANISM      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE      1 (bases 1 to 477)
AUTHORS      Duggal,A.
TITLE      Direct Submission
JOURNAL      Submitted (13-OCT-1995) Arli Duggal, Forestry, Univ. of Toronto, 33
Willcocks St., Toronto, Ont. M5S 3B3, Canada
FEATURES
source      location/Qualifiers
1..477
/organism="Nectria haematococca"
/db_xref="taxon:140110"
1..150
/note="internal transcribed spacer 1; ITS1"
151..306
/product="5.8S ribosomal RNA"
307..477
/note="internal transcribed spacer 2; ITS2"
BASE COUNT      122 a      143 c      114 g      96 t      2 others
ORIGIN

Query Match      100.0%; Score 21; DB 8; Length 477;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactgaga 21
|||||
Db      418 CTACACCTCGCAACTGAGAGA 438

RESULT 7
AF132801      478 bp      DNA      linear      PLN 20-JAN-2000
LOCUS
DEFINITION      Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal
RNA, and internal transcribed spacer 2, complete sequence.
ACCESSION      AF132801
VERSION      AF132801.1 GI:4809015
KEYWORDS
SOURCE      Nectria haematococca.
Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE      1 (bases 1 to 478)
AUTHORS      Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
TITLE      Molecular Identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
JOURNAL      Plant Dis. 84 (1), 83-89 (2000)
2 (bases 1 to 478)
AUTHORS      Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
TITLE      Direct Submission
JOURNAL      Submitted (03-MAR-1999) Plant Pathology, Iowa State University,
Room 351 Bessey Hall, Ames, IA 50011, USA
FEATURES
source      location/Qualifiers
1..478
/organism="Nectria haematococca"
/isolate="P185"
/species="host="Glycine max"
/db_xref="taxon:140110"
/tissue_type="mycelium"
/country="USA: Iowa, Lee County"
1..149
/note="ITS1"
/product="internal transcribed spacer 1"
150..306
/product="5.8S ribosomal RNA"
307..478
/note="ITS2"
/product="internal transcribed spacer 2"
BASE COUNT      123 a      138 c      115 g      102 t      1 others
ORIGIN
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Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttaacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGAGA 439

RESULT 8
AF150459 478 bp DNA linear PLN 05-JAN-2001
LOCUS AF150459
DEFINITION Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150459
VERSION AF150459.1 GI:7650157
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source 1. 478
/organism="Nectria haematococca"
/strain="K-1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
misc_RNA 1. 149
/product="Internal transcribed spacer 1"
rRNA 150..307
/product="5.8S ribosomal RNA"
misc_RNA 308..478
/product="Internal transcribed spacer 2"

BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttaacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGAGA 439

RESULT 9
AF150460 478 bp DNA linear PLN 05-JAN-2001
LOCUS AF150460
DEFINITION Nectria haematococca strain F1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150460
VERSION AF150460.1 GI:7650158
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)

AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source 1. 478
/organism="Nectria haematococca"
/strain="F1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
misc_RNA 1. 149
/product="Internal transcribed spacer 1"
rRNA 150..307
/product="5.8S ribosomal RNA"
misc_RNA 308..478
/product="Internal transcribed spacer 2"

BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttaacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGAGA 439

RESULT 10
AF150461 478 bp DNA linear PLN 05-JAN-2001
LOCUS AF150461
DEFINITION Nectria haematococca strain F4 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150461
VERSION AF150461.1 GI:7650159
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source 1. 478
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/strain="F4"
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/note="anamorph: Fusarium solani"
misc_RNA 1. 149
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rRNA 150..307
/product="5.8S ribosomal RNA"
misc_RNA 308..478
/product="Internal transcribed spacer 2"

BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 11

AF150462 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SW1 internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
AF150462
ACCESSION AF150462.1 GI:7650160
VERSION
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
JOURNAL based on the rDNA-ITS region
REFERENCE Mycol. Res. 104 (10), 1175-1183 (2000)
AUTHORS 2 (bases 1 to 478)
TITLE Suga,H., Hyakumachi,M. and Kageyama,K.
JOURNAL Direct Submission
SUBMITTED (12-MAY-1999) Molecular Genetics Research Center, Gifu
UNIVERSITY, Gifu 501-1112, Japan
LOCATION/Qualifiers

FEATURES
source 1..478
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/strain="SW1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
misc_RNA 1..149
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rRNA 150..307
/product="5.8S ribosomal RNA"
misc_RNA 308..478
/product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 12

AF150463 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF471 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
AF150463
ACCESSION AF150463.1 GI:7650161
VERSION
KEYWORDS Nectria haematococca.
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani

JOURNAL based on the rDNA-ITS region
REFERENCE Mycol. Res. 104 (10), 1175-1183 (2000)
AUTHORS 2 (bases 1 to 478)
TITLE Suga,H., Hyakumachi,M. and Kageyama,K.
JOURNAL Direct Submission
SUBMITTED (12-MAY-1999) Molecular Genetics Research Center, Gifu
UNIVERSITY, Gifu 501-1112, Japan
LOCATION/Qualifiers

FEATURES
source 1..478
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/note="anamorph: Fusarium solani f. sp. radicola"
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/product="internal transcribed spacer 2"
BASE COUNT 123 a 139 c 115 g 101 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.3;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 13

AF150464 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF208 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
AF150464
ACCESSION AF150464.1 GI:7650162
VERSION
KEYWORDS Nectria haematococca.
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
JOURNAL based on the rDNA-ITS region
REFERENCE Mycol. Res. 104 (10), 1175-1183 (2000)
AUTHORS 2 (bases 1 to 478)
TITLE Suga,H., Hyakumachi,M. and Kageyama,K.
JOURNAL Direct Submission
SUBMITTED (12-MAY-1999) Molecular Genetics Research Center, Gifu
UNIVERSITY, Gifu 501-1112, Japan
LOCATION/Qualifiers

FEATURES
source 1..478
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/strain="SUF208"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani f. sp. radicola"
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/product="internal transcribed spacer 1"
rRNA 150..307
/product="5.8S ribosomal RNA"
misc_RNA 308..478
/product="internal transcribed spacer 2"
BASE COUNT 123 a 139 c 115 g 101 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaacactcgcaactggaga 21
|||||
Db 419 CTAACACTCGCACTGGAGA 439

RESULT 14
AF150465 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF532 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF150465
VERSION AF150465.1 GI:7650163
KEYWORDS
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan

FEATURES
source
1. .478
/organism="Nectria haematococca"
/strain="SUF532"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani f. sp. radiclecola"
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1. .149
/product="internal transcribed spacer 1"
rRNA
150. .307
/product="5.8S ribosomal RNA"
308. .478
misc_RNA
/product="internal transcribed spacer 2"
BASE COUNT 124 a 138 c 114 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaacactcgcaactggaga 21
|||||
Db 419 CTAACACTCGCACTGGAGA 439

RESULT 15
AF150469 479 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain MAFF236572 internal transcribed spacer
DEFINITION 1.5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF150469
VERSION AF150469.1 GI:7650167
KEYWORDS
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 479)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)

REFERENCE 2 (bases 1 to 479)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan

FEATURES
source
1. .479
/organism="Nectria haematococca"
/strain="MAFF236572"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani f. sp. piperis"
misc_RNA
1. .151
/product="internal transcribed spacer 1"
rRNA
152. .309
/product="5.8S ribosomal RNA"
310. .479
misc_RNA
/product="internal transcribed spacer 2"
BASE COUNT 120 a 148 c 114 g 97 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 479;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaacactcgcaactggaga 21
|||||
Db 419 CTAACACTCGCACTGGAGA 439

Search completed: August 21, 2002, 22:09:51
Job time: 14205 sec

|

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:47 ; Search time 594.49 Seconds

(without alignments)
60.649 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctacacccgcacgtgaga 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	20	AAV83698
2	21	100.0	319	20	AAV70850
3	19	90.5	502	21	AAV61893
4	19	90.5	561	19	AAV59009
5	17	81.0	510	21	AAV37182
6	17	81.0	2706	21	AAV45891
7	16.2	77.1	33769	22	ABA82622
8	15.8	75.2	1399	23	ABL09973
9	15.8	75.2	1815	23	ABL02977

10	15.8	75.2	3399	23	ABL09972	Drosophila melanog
11	15.8	75.2	3405	24	AAV59263	Long terminal repe
12	15.8	75.2	3947	23	ABL02976	Drosophila melanog
13	15.8	75.2	4334	23	ABL08778	Drosophila melanog
14	15.8	75.2	4763	23	ABL08780	Drosophila melanog
15	15.4	73.3	989	23	ABL18503	Drosophila melanog
16	15.4	73.3	1260	23	ABL11645	Drosophila melanog
17	15.4	73.3	1884	23	AAV55358	Staphylococcus aur
18	15.4	73.3	2310	23	AAV52105	Staphylococcus aur
19	15.4	73.3	2700	23	AAV54538	Staphylococcus aur
20	15.4	73.3	2790	23	AAV55168	Staphylococcus aur
21	15.4	73.3	2853	23	ABL15238	Drosophila melanog
22	15.4	73.3	3061	23	ABL18502	Drosophila melanog
23	15.4	73.3	3433	23	ABL11644	Drosophila melanog
24	15.4	73.3	3713	23	ABL15001	Drosophila melanog
25	15.4	73.3	4676	23	ABL08318	Drosophila melanog
26	15.4	73.3	6325	23	ABL06620	Drosophila melanog
27	15.4	73.3	29555	18	AAV74517	Staphylococcus aur
28	15.4	73.3	41723	23	ABL23684	Drosophila melanog
29	15.2	72.4	352	20	AAV86546	Human single nucle
30	15.2	72.4	352	20	AAV86548	Human single nucle
31	15.2	72.4	352	20	AAV86549	Human single nucle
32	15.2	72.4	351	22	AAV70030	Human immune/haema
33	15.2	72.4	351	22	AAV70031	Human immune/haema
34	15.2	72.4	1173	21	AAV294583	Malze cyclin D ZMC
35	15.2	72.4	1235	22	AAV59374	Human polynucleoti
36	15.2	72.4	1370	21	AAV50337	Arabidopsis thalia
37	15.2	72.4	1609	21	AAV46043	Arabidopsis thalia
38	15.2	72.4	1611	21	AAV33022	Arabidopsis thalia
39	15.2	72.4	1796	22	AAV89924	Human bone marrow
40	15.2	72.4	1800	22	AAV80351	Nucleotide sequenc
41	15.2	72.4	1932	20	AAV19961	Corn cyclin delta-
42	15.2	72.4	2366	23	ABL15104	Drosophila melanog
43	15.2	72.4	2726	22	ABA88958	Escherichia coli p
44	15.2	72.4	3070	23	ABL06688	Escherichia coli p
45	15.2	72.4	13757	22	ABA88957	Escherichia coli p

ALIGNMENTS

RESULT 1	
AAV83698	AAV83698 standard; DNA: 21 BP.
ID	
XX	
AC	AAV83698;
XX	
DT	26-FEB-1999 (first entry)
XX	
DE	Species-specific probe targeted to the internal transcribed spacer 2.
XX	
KW	Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinellioideus; R. circinellioideus; Rhizopus oryzae; R. microsporus;
KW	R. circinellus; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Synthetic.
OS	Fusarium solani.
XX	
FH	Key
FT	modified_base 1
FT	Location/Qualifiers
XX	/*tag- a
XX	/note- "labelled with digoxigenin"
PN	W09850584-A2.
XX	
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	

```

PR 02-MAY-1997; 97US-0045400.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX
DR WPI; 1999-034737/03.
XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Example 1: Page 22; 45pp; English.
XX
CC Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
CC nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
CC plumbeus, M. indicus, M. circinaloides f. circinaloides, Rhizopus
CC pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
CC boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
SQ Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
Db 1 ctacacctgcgaactggaga 21

RESULT 2
AAV70850
ID AAV70850 standard; DNA: 319 BP.
XX
AC AAV70850;
XX
DT 26-FEB-1999 (first entry)
XX
DE Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX
KW Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW M. circinaloides f. circinaloides; Rhizopus oryzae; R. microsporus;
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
OS Fusarium solani.
XX
PN W09850584-A2.
XX
PD 12-NOV-1998.
XX
PP 01-MAY-1998; 98WO-US08926.
XX
PR 02-MAY-1997; 97US-0045400.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX
DR WPI; 1999-034737/03.

```

```

XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Claim 1: Page 12; 45pp; English.
XX
CC The present sequence represents an internal transcribed spacer 2 (ITS2)
CC and adjacent regions. Probes can be derived from the present sequence
CC which are species-specific. The specification also describes ITS2
CC sequence-derived probes for identifying a species selected from
CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinaloides f. circinaloides, Rhizopus oryzae,
CC Absidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
CC (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
SQ Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
Db 222 ctacacctgcgaactggaga 242

RESULT 3
AAA61893
ID AAA61893 standard; DNA: 502 BP.
XX
AC AAA61893;
XX
DT 14-NOV-2000 (first entry)
XX
DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX
KW Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
KW HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
KW acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
KW symptomatic infection; asymptomatic infection; potential HIV exposure;
KW combination therapy; ds.
XX
OS Fusarium sp. MF6381.
XX
PN W0200036132-A1.
XX
PD 22-JUN-2000.
XX
PP 09-DEC-1999; 99WO-US29356.
XX
PR 14-DEC-1998; 98US-0112168.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
XX
PI Dombrowski AW;
XX
DR WPI; 2000-431606/37.
XX
PT New steroid compounds are HIV integrase inhibitors used for treating
PT HIV infection and AIDS -
XX
PS Disclosure: Page 14; 113pp; English.
XX
CC The invention relates to novel steroid compounds derived from the

```

CC African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as
CC inhibitors of HIV integrase. The invention encompasses cultures of
CC *Fusarium* sp. MF6381. The invention also relates to a composition
CC comprising a compound of the invention in combination with an AIDS
CC antiviral agent, an immunomodulator and an anti-infective agent. The
CC compounds of the invention may be used in the inhibition of HIV
CC integrase and in the prevention and treatment of HIV infection. A wide
CC range of state of HIV infection may be treated: AIDS (acquired
CC immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic
CC and asymptomatic HIV infection; and actual or potential exposure to HIV.
CC The compounds may be used to isolate HIV integrase mutants which are
CC potentially useful as screening tools for antiviral compounds. The
CC compounds may also be used to establish or determine the site at which
CC other antivirals bind to HIV integrase (e.g., by competitive inhibition).
CC The present sequence represents the ribosomal DNA (rDNA) internal
CC transcribed spacer (ITS) region of *Fusarium* sp. MF6381, which may be used
CC to characterise MF6381.

SO Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 other;

Query Match 90.5%; Score 19; DB 21; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacacctcgcaactgga 19
|||||
Db 410 ctacacctcgcaactgga 428

RESULT 4

AAV59009
ID AAV59009 standard; DNA: 561 BP.

XX AAV59009;

DT 06-JAN-1999 (first entry)

XX F. avenaceum internal transcribed spacer.

XX Internal transcribed spacer; ITS; Microdochium; *Fusarium*; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.

XX *Fusarium avenaceum*.

XX Key Location/Qualifiers

FT misc_feature 31..181

FT /tag- a
FT /note- "ITS1"

FT misc_feature 339..504

FT /tag- b
FT /note- "ITS2"

XX US5827695-A.

PD 27-OCT-1998.

XX 01-AUG-1997; 97US-0905314.

XX 01-AUG-1997; 97US-0905314.

XX (NOVS) NOVARTIS FINANCE CORP.

XX Beck JJ;

XX WPI; 1998-593995/50.

XX Wheat pathogen internal transcribed spacer sequences - used as a
PT basis for primers for the species-specific polymerase chain reaction
PT detection of the pathogens

PS Claim 1; Column 29-30; 20pp; English.

CC This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*,
CC *F. avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.

SO Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 3 other;

Query Match 90.5%; Score 19; DB 19; Length 561;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacacctcgcaactgga 19
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Db 445 ctacacctcgcaactgga 463

RESULT 5

AAC37182
ID AAC37182 standard; DNA: 510 BP.

XX AAC37182;

XX 17-OCT-2000 (first entry)

XX *Arabidopsis thaliana* DNA fragment SEQ ID NO: 16470.

KM Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX *Arabidopsis thaliana*.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 29-MAR-1999; 99US-0126264.

XX 01-APR-1999; 99US-0126785.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

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XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 04-MAY-1999; 99US-0132047.

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XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

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XX 19-MAY-1999; 99US-0134768.

XX 20-MAY-1999; 99US-0134941.

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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 31-AUG-1999; 99US-0151348.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 04-OCT-1999; 99US-0157117.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
Query Match 81.0%; Score 17; DB 21; Length 510;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 caccctgcgaactggaga 21
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DB 37 caccctgcgaactggaga 53
RESULT 6
AAC45891
ID AAC45891 standard; DNA; 2706 BP.
XX
XX AAC45891;
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 48143.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EP103405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 21-JUL-1999; 99US-0145086.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 05-OCT-1999; 99US-0157753.
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PR 07-OCT-1999; 99US-0158029.
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PR 28-OCT-1999; 99US-0161892.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 81.0%; Score 17; DB 21; Length 2706;
Best Local Similarity 100.0%; Pred. No. 41;

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 caccctgcactgcagaga 21
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Db 20 caccctgcactgcagaga 36
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RESULT 7
ABA82622
ID ABA82622 standard; DNA: 33769 BP.
XX
AC ABA82622;
DT 25-JAN-2002 (first entry)
XX
DE Human HBM gene region b527d12-h_contig308G.
XX
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KM Human; high bone mass; HBM gene; zmx1 gene; chromosome 11; 11q13.3;
KM sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KM antisenese therapy; vaccine; bone disorder; Paget's disease;
KM sclerostosis; osteomalacia; fibrous dysplasia; ds.
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OS Homo sapiens.

PN WO200177327-A1.

PD 18-OCT-2001.

PF 21-JUN-2000; 2000WO-US16951.

PR 05-APR-2000; 2000US-0543771.

PR 05-APR-2000; 2000US--0544398.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Carulla JF, Little RD, Recker RR, Johnson ML;

XX WPI; 2001-657171/75.

XX New high bone mass (HBM) and zmx1 genes and proteins useful for

PT modulating bone mass for the treatment of e.g. osteoporosis -

XX Claim 51; Page 237-257; 443pp; English.

XX The present invention describes the human zmx1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The zmx1 and
CC HBM genes have osteopathic activities. The genes can be used in gene
CC therapy, antisenese therapy and in the production of vaccines. They
CC can be used in the diagnosis and treatment of bone disorders including
CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous
CC dysplasia. ABA82038 to ABA82760 and AAC68168 to AAC68193 represent
CC sequences used in the exemplification of the present invention.

XX Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 3 other:

Query Match 77.1%; Score 16.2; DB 22; Length 33769;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ctaacactgcactgcagaga 21

Db 25831 ctaacactgcactgcagaga 25851

RESULT 8

ABL09973

ID ABL09973 standard; cDNA: 1399 BP.

XX ABL09973;

DT 26-MAR-2002 (first entry)

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DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24401.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PP 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR P-PSDB; ABB65870.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 24401; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1399 BP; 387 A; 361 C; 338 G; 313 T; 0 other;
SQ
Query Match 75.2%; Score 15.8; DB 23; Length 1399;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 taacacctgcgaactgag 20
1 ||||| ||||| |||||
DB 75 tgcacccgcgaactgag 93
RESULT 9
AB102977
ID ABL02977 standard; cDNA; 1815 BP.
XX
XX ABL02977;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 3413.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF

```

```

XX
XX 23-MAR-2000; 2000US-191637P.
PR
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB58874.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 3413; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1815 BP; 462 A; 488 C; 557 G; 308 T; 0 other;
SQ
Query Match 75.2%; Score 15.8; DB 23; Length 1815;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 aacacctgcgaactgaga 21
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DB 559 agcacatgcgaactgaga 577
RESULT 10
AB109972
ID ABL09972 standard; cDNA; 3399 BP.
XX
XX ABL09972;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24398.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB65869.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT

```


Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 aacacctgcgaactggaga 21
1 ||||| ||||| ||||| |||||
Db 1559 agcacatcgcaactggaga 1577

RESULT 13

ABL08778
ID ABL08778 standard; cDNA: 4394 BP.

ABL08778;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 20816.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PMD, Myers EW;

WPI: 2001-656860/75.

P-PSDB; ABB64675.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 20816; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4394 BP; 1217 A; 1007 C; 1015 G; 1155 T; 0 other;

Query Match 75.2%; Score 15.8; DB 23; Length 4394;

Best Local Similarity 89.5%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 taacacctgcgaactggag 20
1 ||||| ||||| ||||| |||||

Db 208 tgcaccccgcaactggag 226

RESULT 14

ABL08780
ID ABL08780 standard; cDNA: 4763 BP.

ABL08780;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 6982.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ds.

Drosophila melanogaster.

WO200171042-A2.

ABL08780;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 20822.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PMD, Myers EW;

WPI: 2001-656860/75.

P-PSDB; ABB64677.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 20822; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4763 BP; 1170 A; 1167 C; 1147 G; 1279 T; 0 other;

Query Match 75.2%; Score 15.8; DB 23; Length 4763;

Best Local Similarity 89.5%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 taacacctgcgaactggag 20
1 ||||| ||||| ||||| |||||

Db 4132 tgcaccccgcaactggag 4150

RESULT 15

ABL18503/c
ID ABL18503 standard; DNA: 989 BP.

ABL18503;

26-MAR-2002 (first entry)

Drosophila melanogaster genomic polynucleotide SEQ ID NO 6982.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ds.

Drosophila melanogaster.

WO200171042-A2.

XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PA
XX (PEKE) PE CORP NY.
PI
XX Venter JC, Adams M, Li PWD, Myers EW;
DR WPI: 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1; SEQ ID NO 6982; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU1840-ABU16175) and the encoded proteins
(ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 989 BP; 228 A; 245 C; 234 G; 282 T; 0 other;

Query Match 73.3%; Score 15.4; DB 23; Length 989;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 acactcgcaactggag 20
|||||
DB 191 ACACCTCGCACTGGAG 175

Search completed: August 21, 2002, 22:22:51
Job time: 5791 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:27 ; Search time 5019.06 Seconds
(without alignments)
56.472 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21
1 ctcaacctgcgaactggaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gD_estl:*
10: gD_estl2:*
11: gD_hic:*
12: gD_gsa:*
13: em_gsa_hum:*
14: em_gsa_huv:*
15: em_gsa_pin:*
16: em_gsa_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.8	80.0	362	9	BE070797 RC3-BT050
2	16.8	80.0	458	12	AO681735 HS_2142_A
3	16.8	80.0	552	12	A2191211 SP_1019_A
4	16.8	80.0	610	10	BM440563 pgrin.pk0
5	16.8	80.0	972	12	CNS0777X
6	16.8	80.0	1321	10	BT490849 603031810
7	16.4	78.1	174	9	AT001540
8	16.4	78.1	300	9	AT019460
9	16.4	78.1	376	9	AV191390 AV191390
10	16.4	78.1	380	10	BJ154339 BJ154339
11	16.4	78.1	394	10	BJ125969 BJ125969
12	16.4	78.1	469	9	AM582687 RC0-ST029
13	16.4	78.1	586	9	AU218686 AU218686
14	16.4	78.1	587	10	BF619904 HVSMEC000
15	16.4	78.1	713	12	BH064238 RPCT-24-3
16	16.4	78.1	787	12	BH061459 RPCT-24-3
17	16.4	78.1	819	12	BH061403 RPCT-24-3

C 18	16.2	77.1	252	12	A2468148
C 19	16.2	77.1	266	9	AV043034
C 20	16.2	77.1	293	9	BB089128
C 21	16.2	77.1	293	9	BB572305
C 22	16.2	77.1	326	12	A0260963
C 23	16.2	77.1	349	12	A0013861
C 24	16.2	77.1	430	12	A0836420
C 25	16.2	77.1	437	9	AA840330
C 26	16.2	77.1	439	9	AM081834
C 27	16.2	77.1	452	10	BF320988
C 28	16.2	77.1	492	12	A0585499
C 29	16.2	77.1	494	10	W45853
C 30	16.2	77.1	497	12	A0138222
C 31	16.2	77.1	513	9	AA530317
C 32	16.2	77.1	521	9	AM701534
C 33	16.2	77.1	547	9	AL601781
C 34	16.2	77.1	579	12	A2965522
C 35	16.2	77.1	648	12	AG106800
C 36	16.2	77.1	659	9	BE198784
C 37	16.2	77.1	803	10	BG285094
C 38	16.2	77.1	839	10	BG872601
C 39	16.2	77.1	974	10	BI415029
C 40	16.2	77.1	998	10	BG622763
C 41	16.2	77.1	1101	12	CNS00025
C 42	16.2	77.1	1519	9	AM727720
C 43	16.2	77.1	1539	10	BI160925
C 44	16.2	77.1	1903	11	AK015469
C 45	16.2	77.1	3073	11	AK004854

ALIGNMENTS

RESULT	LOCUS	DEPOSITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1	BE070797	RC3-BT0502-251199-011-b12	BT0502	Homo sapiens	CDNA, mRNA sequence.	EST. 09-JUN-2000	362 bp	1					
	BE070797	BE070797.1	GI:8415443				Homo sapiens						
							human.						
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
							1 (bases 1 to 362)						
							Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.U.						
							Shotgun sequencing of the human transcriptome with ORF expressed sequence tags						
							Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
							Contact: Simpson A.U.G.						
							Laboratory of Cancer Genetics						
							Ludwig Institute for Cancer Research						
							Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil						
							Tel: +55-11-3704922						
							Fax: +55-11-3707001						
							Email: asimpson@ludwig.org.br						
							This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL						
							(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC3-BT0502-251199-011-b12&t3=1999-11-25&t4=1)						
							Seq primer: puc 18 forward						
							High quality sequence start: 28						
							High quality sequence stop: 362.						
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							1. 362						
							/organism="Homo sapiens"						

/db_xref="taxon:9606"
 /clone_lib="BT0502"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ONESTEPS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 82 a 120 c 47 g 113 t

Query Match 80.0%; Score 16.8; DB 9; Length 362;
 Best Local Similarity 90.0%; Pred. No. 4.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ctacacactgcgaactgag 20
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 Db 39 CTAACTTCTCGCACTGAG 58

RESULT 2
 LOCUS AO681735 458 bp DNA linear GSS 28-JUN-1999
 DEFINITION HS_2142_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2142 Col=8 Row=1, DNA sequence.
 ACCESSION AO681735
 VERSION AO681735.1 GI:52527718
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 458)
 Mahairas,G.G., Wallace,J.C., Smith,R., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.husc.washington.edu
 Plate: 2142 row: 1 column: 8
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 458.
 Location/Qualifiers
 1 458
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate=2142 Col=8 Row=1"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 114 a 122 c 106 g 109 t 7 others
 ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 458;
 Best Local Similarity 90.0%; Pred. No. 5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ctacacactgcgaactgag 20
 ||||| ||||| ||||| |||||
 Db 439 CTAACTTCTCGCACTGAG 458

RESULT 3
 LOCUS A2191211 552 bp DNA linear GSS 30-AUG-2000
 DEFINITION SP_1019_A1_A04_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1019 Col=7 Row=A, DNA sequence.
 ACCESSION A2191211
 VERSION A2191211.1 GI:8374390
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus.
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 552)
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 A sea urchin genome project: Sequence scan, virtual map, and additional resources
 Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
 20402566
 Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 1019 row: A column: 7
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 552.
 Location/Qualifiers
 1 552
 /organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
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 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"

BASE COUNT 173 a 106 c 105 g 164 t 4 others
 ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 552;
 Best Local Similarity 85.7%; Pred. No. 5.3e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ctacacactgcgaactgaga 21
 ||| ||||| ||||| |||||
 Db 407 CTAGACCTCGNATCTGAGA 427

RESULT 4
 LOCUS BM440563 610 bp mRNA linear EST 01-FEB-2002
 DEFINITION pgrih.pk003.h4 Normalized Chicken Reproductive Tract cDNA Library (pgrih) Gallus gallus cDNA clone pgrih.pk003.h4 5' similar to no significant hits (plog(p) 4), mRNA sequence.
 ACCESSION BM440563
 VERSION BM440563.1 GI:18471338
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 610)
Cogburn, L.A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry unit Project
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburnudel.edu, www.chickest.udel.edu.
Location/Qualifiers

FEATURES
source
1. 610
/organism="Gallus gallus"
/strain="Commercial broiler and layer"
/db_xref="taxon:9031"
/clone="pgrln.pk003.h4"
/clone_lib="Normalized Chicken Reproductive Tract cDNA
library (pgrln)"
/sex="Male and Female"
/tissue_type="Testis, ovary and oviduct"
/dev_stage="Various stages; embryonic, post-hatch, immature
and sexually-mature"
/lab_host="E. coli EMDH108"
/note="Vector: PCMVSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
oviduct 50% of final RNA pool); Single pass sequencing
from 5'-end"

BASE COUNT
148 a 145 c 141 g 176 t

ORIGIN

Query Match
Best Local Similarity 90.0%; Score 16.8; DB 10; Length 610;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 taacacctgcgaactggaga 21
|||||
Db 550 TAAGACCTCGCAATGAGAGA 569

RESULT 5
CNS0777Y 972 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BB0AA009H05 of library BB0AA from strain CBS 4732
DEFINITION of *Pichia angusta*, genomic survey sequence.
ACCESSION AL432356
VERSION AL432356.1 GI:12215770
KEYWORDS GSS.
SOURCE *Pichia angusta*.
ORGANISM *Pichia angusta*.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; *Pichia*.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 972)
Blandin, G., Florente, B., Malpertuy, A., Wincker, P., Artiguenave, F.
and Dujon, B.
Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*
angusta
FEMS Lett. 487 (1), 76-81 (2000)
2 (bases 1 to 972)
Soucier, J.L., Algle, M., Artiguenave, F., Blandin, G.,
Biolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Florente, B.,
Malpertuy, A., Neveuglise, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
20584711

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

3 (bases 1 to 972)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marianus* var. *marianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Location/Qualifiers

FEATURES
source
1. 972
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA009H05"
/clone_lib="BB0AA"
/note="end : 77"

BASE COUNT
289 a 247 c 236 g 198 t 2 others

ORIGIN

Query Match
Best Local Similarity 90.0%; Score 16.8; DB 12; Length 972;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 taacacctgcgaactggaga 21
|||||
Db 772 TAACACCTCGCAAGAGAGA 791

RESULT 6
BI490849 1321 bp mRNA linear EST 28-AUG-2001
LOCUS 603031810T1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172818 3',
DEFINITION mRNA sequence.
ACCESSION BI490849
VERSION BI490849.1 GI:15330077
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1321)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11430 row: d column: 03
High quality sequence stop: 749.
Location/Qualifiers

FEATURES
source
1. 1321
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5172818"
/clone_lib="NIH_MGC_115"
/lab_host="DH108"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

BASE COUNT 363 a 310 c 430 g 218 t
ORIGIN

Query Match 80.0%; Score 16.8; DB 10; Length 1321;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 taacactgcgaactggaga 21
||||| ||||| |||||
Db 1262 TAACACCACGACACGAGA 1281

RESULT 7
AT001540 174 bp mRNA linear EST 26-MAR-1999
LOCUS AT001540 Acanthamoeba healyi CDNA library Acanthamoeba healyi CDNA
DEFINITION clone Ahc507, mRNA sequence.
ACCESSION AT001540 GI:4528633
VERSION AT001540.1 GI:4528633
KEYWORDS EST.
SOURCE Acanthamoeba healyi.
ORGANISM Acanthamoebidae; Acanthamoeba.

REFERENCE 1 (bases 1 to 174)
AUTHORS Kong,H.H., Hwang,M.Y., Yu,H.S., Hong,Y.C., Kim,T.O. and Chung,D.I.

TITLE New insight into biology of Acanthamoeba healyi by expressed
sequence tag analysis
JOURNAL Unpublished (1999)
COMMENT Contact: Kong HH

Department of Parasitology
Kyungpook National University School of Medicine
101 Dongin-dong, Chung-ku, Taegu 700 - 422, Korea
Email: hhkong@bh.kyungpook.ac.kr.

FEATURES
source Location/Qualifiers

1..174
/organism="Acanthamoeba healyi"
/strain="QC-3A"
/db_xref="taxon:65661"
/clone="ahc507"
/clone_lib="Acanthamoeba healyi CDNA library"
/dev_stage="trophozoite"

BASE COUNT 38 a 52 c 52 g 32 t
ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 174;
Best Local Similarity 94.4%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 aacactgcgaactggaga 21
||||| ||||| |||||
Db 25 ACACCTCGCAACTGGAGA 42

RESULT 8
AV179460 300 bp mRNA linear EST 21-JUL-1999
LOCUS AV179460 C
DEFINITION AV179460 Yuj1 Kohara unpublished CDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans CDNA clone YK593d12 3', mRNA
sequence.
ACCESSION AV179460
VERSION AV179460.1 GI:5559361
KEYWORDS EST.
SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Shin-I,Y., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuj1 Kohara
Genome Biology Lab.

National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source Location/Qualifiers

1..300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk593d12"
/clone_lib="Yuj1 Kohara unpublished CDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 76 a 65 c 71 g 85 t 3 others
ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 300;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 aacactgcgaactggag 20
||||| ||||| |||||
Db 199 AACACTCGCAACTGGAG 182

RESULT 9
AV191390 376 bp mRNA linear EST 22-JUL-1999
LOCUS AV191390
DEFINITION AV191390 Yuj1 Kohara unpublished CDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans CDNA clone YK593d12 5', mRNA
sequence.

ACCESSION AV191390
VERSION AV191390.1 GI:5573542
KEYWORDS EST.
SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 376)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuj1 Kohara
Genome Biology Lab.

National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source Location/Qualifiers

1..376

/organism="Caenorhabditis elegans"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk593d12"

/clone_lib="yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 117 a 85 c 94 g 80 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 376;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 aacacctgcgaactggag 20
||||| |||||||

DB 313 AACACTTCGCAACTGCAG 330

RESULT 10
BJ154339 380 bp mRNA linear EST 24-JAN-2002
LOCUS BJ154339 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1329g02 3', mRNA sequence.
ACCESSION BJ154339
VERSION BJ154339.1 GI:18322324
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 380)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1. .380
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 108 a 72 c 87 g 113 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 10; Length 380;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 aacacctgcgaactggag 20
||||| |||||||

DB 255 AACACTTCGCAACTGCAG 238

RESULT 11
BJ125969 394 bp mRNA linear EST 23-JAN-2002
LOCUS BJ125969 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1329g02 5', mRNA sequence.
ACCESSION BJ125969
VERSION BJ125969.1 GI:18286116
KEYWORDS EST.

SOURCE
ORGANISM Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 394)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1. .394
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 123 a 88 c 72 g 111 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 10; Length 394;
Best Local Similarity 94.4%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 aacacctgcgaactggag 20
||||| |||||||

DB 126 AACACTTCGCAACTGCAG 143

RESULT 12
AWS82687 469 bp mRNA linear EST 16-MAR-2000
LOCUS AWS82687
DEFINITION RC0-ST0299-070100-011-g06 ST0299 Homo sapiens cDNA, mRNA sequence.
ACCESSION AWS82687
VERSION AWS82687.1 GI:7257736
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&c2=RC0-ST0299-
070100-011-g06&c3=2000-01-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 55
High quality sequence stop: 195.
location/Qualifiers
1. .469
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone_lib="ST0299"
/dev_stage="Adult"
/note="organ: stomach; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 141 a 120 c 123 g 85 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 469;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 aacacctgcgaactggag 20
||||| |||||||

Db 354 AACACTGCAACTGAG 371

RESULT 13
AU218666 586 bp mRNA linear EST 17-JUL-2001
LOCUS AU218666
DEFINITION AU218666 unpublished oligo-capped cDNA library, stage 1
Caenorhabditis elegans cDNA clone yk867e09 3', mRNA sequence.
ACCESSION AU218666
VERSION AU218666.1 GI:14856823
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 586) Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2001)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..586
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk867e09"
/clone_lib="unpublished oligo-capped cDNA library, stage
1"
/sex="Hermaphrodite"
/tissue="whole animal"
/dev_stage="1"

BASE COUNT 153 a 126 c 135 g 171 t 1 others

ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 586;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 aacacctgcgaactggag 20
||||| |||||||

Db 247 AACACTGCAACTGAG 230

RESULT 14
BF619904

LOCUS BF619904 587 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMC0009K02f Hordeum vulgare seedling shoot EST library
HVCNNA0003 (Etisolated and unstressed) Hordeum vulgare cDNA clone
HVSMC0009K02f, mRNA sequence.
ACCESSION BF619904
VERSION BF619904.2 GI:13107889
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 587)
Wing, R., Close, T. J., Kleinof, A., Wise, R., Begum, D., Fritsch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton
, R. D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling shoot cDNA library
Unpublished (2001)
On Dec 18, 2000 this sequence version replaced gi:11883638.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 393
Seq primer: AATTAACTCCTCACTAAGGC
High quality sequence stop: 576.
Location/Qualifiers
1..587
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMC0009K02f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCNNA0003 (Etisolated and unstressed)"
/tissue="type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP. Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedling shoots were
then harvested. Total RNA was prepared. poly(A) RNA was
purified. One primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give plasmid
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinof A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 163 a 117 c 171 g 136 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 10; Length 587;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 aacctgcgaactggag 20
 |||||
 Db 96 AACACCTGCTACTGGAG 113

RESULT 15

BH064238 713 bp DNA linear GSS 18-JUL-2001
 LOCUS BH064238/c
 DEFINITION RPI-24-370K21.TV RPI-24 Mus musculus genomic clone RPI-24-370K21
 , DNA sequence.

ACCESSION BH064238
 VERSION BH064238.1 GI:14879771
 KEYWORDS GSS.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
 Tsagaye,G., Geer,K., Krol,M., Shwartsbeyn,A., Gebregeorgis,E.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPI-24
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT Other GSSs: RPI-24-370K21.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhaotlgr.org

Clones are derived from the mouse BAC library RPI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tlgr.org/tlgr/bac_ends/mouse/bac_end_intro.html
 Plate: 370 row: K column: 21
 Seq primer: 77

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..713
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPI-24-370K21"
 /clone_id="RPI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTARBAC1. Site 1: BamHI. Site 2: BamHI.
 RPI-24 Mouse BAC Library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT 170 a 157 c 175 g 211 t
 ORIGIN

Query Match 78.1%; Score 16.4; DB 12; Length 713;

Best Local Similarity 94.4%; Pred. NO. 9.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 aacctgcgaactggag 21
 |||||
 Db 463 ACACCTGCACTGGAGA 446

Search completed: August 21, 2002, 21:32:34
 Job time: 12533 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:12:32 ; Search time 138.45 Seconds
(without alignments)
37.238 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaccactcgcacactgaga 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCrnu.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	90.5	561	1 US-08-905-314A-24	Sequence 24, Appl
2	14.6	69.5	517	4 US-09-276-531-122	Sequence 122, App
3	14.6	69.5	1766	5 PCT-US93-00601-1	Sequence 1, Appl1
4	14.6	69.5	1766	5 PCT-US94-07107A-1	Sequence 1, Appl1
5	14.6	69.5	1767	4 US-08-083-945C-1	Sequence 1, Appl1
6	14.6	69.5	1784	1 US-08-554-612C-13	Sequence 13, Appl1
7	14.6	69.5	2636	1 US-08-554-612C-12	Sequence 12, Appl1
8	14.6	69.5	2898	1 US-08-554-612C-51	Sequence 51, Appl1
9	14.6	69.5	2909	1 US-08-554-612C-10	Sequence 10, Appl1
10	14.6	69.5	2909	1 US-08-554-612C-11	Sequence 11, Appl1
11	14.6	69.5	5843	1 US-08-554-612C-2	Sequence 2, Appl1
12	14.2	67.6	644	4 US-09-386-493-9	Sequence 9, Appl1
13	14.2	67.6	1095	4 US-08-928-383B-3	Sequence 3, Appl1
14	14.2	67.6	1584	4 US-08-928-383B-1	Sequence 1, Appl1
15	14.2	67.6	2434	4 US-09-272-496-1	Sequence 1, Appl1
16	14.2	67.6	2601	4 US-08-569-749-3	Sequence 3, Appl1
17	14.2	67.6	2601	5 PCT-US96-12860-3	Sequence 3, Appl1
18	14.2	67.6	2676	2 US-08-511-485-5	Sequence 5, Appl1
19	14.2	67.6	3076	2 US-09-205-144-1	Sequence 1, Appl1
20	14.2	67.6	3416	2 US-08-724-394A-15	Sequence 15, Appl1
21	14.2	67.6	3463	4 US-09-189-462-3	Sequence 3, Appl1
22	14.2	67.6	4131	1 US-08-485-588-4	Sequence 4, Appl1
23	14.2	67.6	4131	2 US-08-484-565-4	Sequence 4, Appl1
24	14.2	67.6	4131	2 US-08-480-751-4	Sequence 4, Appl1
25	14.2	67.6	4131	2 US-08-943-986-4	Sequence 4, Appl1
26	14.2	67.6	4131	3 US-08-353-784-4	Sequence 4, Appl1
27	14.2	67.6	4131	3 US-08-484-719B-4	Sequence 4, Appl1

c 28	14.2	67.6	4131	4 US-08-484-159-4	Sequence 4, Appl1
c 29	14.2	67.6	4768	1 US-07-596-467-1	Sequence 1, Appl1
c 30	14.2	67.6	4768	1 US-07-934-374-1	Sequence 1, Appl1
c 31	14.2	67.6	4768	1 US-07-783-861C-3	Sequence 3, Appl1
c 32	14.2	67.6	5115	3 US-08-348-518C-3	Sequence 3, Appl1
c 33	14.2	67.6	5115	3 US-08-476-509B-3	Sequence 3, Appl1
c 34	14.2	67.6	6669	3 US-09-212-971-5	Sequence 5, Appl1
c 35	14.2	67.6	6669	3 US-08-800-929A-5	Sequence 5, Appl1
c 36	14.2	67.6	6669	4 US-09-617-053A-5	Sequence 5, Appl1
c 37	13.8	65.7	405	6 5171839-1	Patent No. 5171839
c 38	13.8	65.7	525	3 US-08-911-853-18	Sequence 18, Appl1
c 39	13.8	65.7	525	4 US-09-479-409-18	Sequence 18, Appl1
c 40	13.8	65.7	525	4 US-09-479-453-18	Sequence 18, Appl1
c 41	13.8	65.7	780	1 US-08-325-553-27	Sequence 27, Appl1
c 42	13.8	65.7	780	2 US-08-394-152A-27	Sequence 27, Appl1
c 43	13.8	65.7	2272	1 US-08-482-577B-1	Sequence 1, Appl1
c 44	13.8	65.7	2272	3 US-08-289-222E-2	Sequence 2, Appl1
c 45	13.8	65.7	2272	4 US-09-218-176-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-905-314A-24
Sequence 24, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NO. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..181

OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note="5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 90.5%: Score 19; DB 1; Length 561;
Best Local Similarity 100.0%: Pred. No. 0.36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgga 19
|||||
DB 445 CTAACACCTCGCAACTGGA 463

RESULT 2
US-09-276-531-122
Sequence 122, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
NUMBER OF SEQUENCES: 134
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murty, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGSTUT08
CLONE: 2642108
US-09-276-531-122

Query Match 69.5%: Score 14.6; DB 4; Length 517;
Best Local Similarity 81.0%: Pred. No. 70;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgga 21
|||||
DB 442 CTAACACTTGTACTGAGGA 462

RESULT 3
PCT-US93-00601-1
Sequence 1, Application PC/TUS9300601
GENERAL INFORMATION:
APPLICANT: Becker, Marie E.
APPLICANT: Liotta, Lance A.
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00601
FILING DATE: 19930129
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1766 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 35..1279
PCT-US93-00601-1

Query Match 69.5%: Score 14.6; DB 5; Length 1766;
Best Local Similarity 81.0%: Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgga 21
|||||
DB 66 CTGACACCCCGCCTGAGGA 86

RESULT 4
PCT-US94-07107A-1
Sequence 1, Application PC/TUS9407107A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of
APPLICANT: America, as represented by the Secretary,
Department of Health and Human Services
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 15

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07107A
FILING DATE: 25-JUN-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1766 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 34..1278
PCT-US94-07107A-1

Query Match          69.5%; Score 14.6; DB 5; Length 1766;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctacaccctgcgaactggaga 21
   ||||||| | |||||||
Db 66 CTGACACCCCTGAGAGAGA 86

RESULT 5
US-08-083-945C-1
; Sequence 1, Application US/08083945C
; Patent No. 6274134
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kutzsch, Henry C.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,945C
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: C-DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1336
US-08-083-945C-1

Query Match          69.5%; Score 14.6; DB 4; Length 1767;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctacaccctgcgaactggaga 21
   ||||||| | |||||||
Db 66 CTGACACCCCTGAGAGAGA 86

RESULT 6
US-08-554-612C-13/C
; Sequence 13, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orlicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660emder 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1784 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-554-612C-13
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Query Match 69.5%; Score 14.6; DB 1; Length 1784;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctaacacctgcgaactggaga 21
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Db 1099 CTAACATCTCGCACCAGTAGA 1079

RESULT 7

US-08-554-612C-12/C
; Sequence 12, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orllicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660ember 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ. ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-554-612C-12

Query Match 69.5%; Score 14.6; DB 1; Length 2636;
Best Local Similarity 81.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctaacacctgcgaactggaga 21
||||| ||||| |||||
Db 1099 CTAACATCTCGCACCAGTAGA 1079

RESULT 8

US-08-554-612C-51/C
; Sequence 51, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orllicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ. ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-554-612C-51

Query Match 69.5%; Score 14.6; DB 1; Length 2898;
Best Local Similarity 81.0%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctaacacctgcgaactggaga 21
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Db 1088 CTAACATCTCGCACCAGTAGA 1068

RESULT 9
US-08-554-612C-10/C
; Sequence 10, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orllicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660ember 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ. ID NO: 10:
; SEQUENCE CHARACTERISTICS:

LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-10

Query Match 69.5%; Score 14.6; DB 1; Length 2909;
Best Local Similarity 81.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
||||| ||||| |||||
Db 1099 ctaacacctgcgaactggaga 1079

RESULT 10
US-08-554-612C-11/C
Sequence 11, Application US/08554612C
Patent No. 5747660

GENERAL INFORMATION:
APPLICANT: Orlicky, David
TITLE OF INVENTION: PROTAGLANDIN F2 RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-11

Query Match 69.5%; Score 14.6; DB 1; Length 2909;
Best Local Similarity 81.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 1099 ctaacacctgcgaactggaga 1079

RESULT 11
US-08-554-612C-2/C
Sequence 2, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:

APPLICANT: Orlicky, David
TITLE OF INVENTION: PROTAGLANDIN F2 RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-2

Query Match 69.5%; Score 14.6; DB 1; Length 5843;
Best Local Similarity 81.0%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 1137 ctaacacctgcgaactggaga 1117

RESULT 12
US-09-386-493-9
Sequence 9, Application US/09386493
Patent No. 6262247

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Azimzal, Yalda
TITLE OF INVENTION: POLYCYCLIC AROMATIC HYDROCARBON INDUCED MOLECULES
FILE REFERENCE: PB-0011 US
CURRENT APPLICATION NUMBER: US/09/386,493
CURRENT FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 9

LENGTH: 644
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: unsure
LOCATION: 44

OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE:
NAME/KEY:
OTHER INFORMATION: 700062690
PUBLICATION INFORMATION:
US-09-386-493-9

Query Match 67.6%; Score 14.2; DB 4; Length 644;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||| |||||
Db 176 taacacatgcacatgag 194

RESULT 13

US-08-928-383B-3/C
; Sequence 3, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Flinberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026.100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
US-08-928-383B-3

Query Match 67.6%; Score 14.2; DB 4; Length 1095;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||||| ||| ||
Db 440 TAACATCTCGCACCCTGAG 422

RESULT 14

US-08-928-383B-1/C
; Sequence 1, Application US/08928383B
; Patent No. 6210921

; GENERAL INFORMATION:
; APPLICANT: Robert W. Flinberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026.100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..1157
US-08-928-383B-1

Query Match 67.6%; Score 14.2; DB 4; Length 1584;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||||| ||| ||
Db 499 TAACATCTCGCACCCTGAG 481

RESULT 15

US-09-272-496-1/C
; Sequence 1, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272.496
; EARLIER APPLICATION NUMBER: 1999-03-19
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

: NAME/KEY: CDS
: LOCATION: (60)..(1154)
US-09-272-496-1

Query Match 67.68; Score 14.2; DB 4; Length 2434;
Best Local Similarly 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 taacacctgcgaactggag 20
Db 499 TAACATCTGCACCTGAG 481

Search completed: August 21, 2002, 22:12:34
Job time: 5707 sec

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: August 22, 2002, 00:39:40 ; Search time 8184.59 Seconds
(without alignments)
55.511 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctacacctgcgaactgaga 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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13: /cgn2_6/ptodata/1/pna/US089_COMB.seq.*

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17: /cgn2_6/ptodata/1/pna/US093_COMB.seq.*

18: /cgn2_6/ptodata/1/pna/US094_COMB.seq.*

19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq.*

20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq.*

21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq.*

22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq.*

23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq.*

24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*

25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq.*

26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*

27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*

28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*

29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*

30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*

31: /cgn2_6/ptodata/1/pna/US098A_COMB.seq.*

32: /cgn2_6/ptodata/1/pna/US098B_COMB.seq.*

33: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*

34: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*

35: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*

36: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*

37: /cgn2_6/ptodata/1/pna/US100_COMB.seq.*

38: /cgn2_6/ptodata/1/pna/US101_COMB.seq.*

39: /cgn2_6/ptodata/1/pna/US6000_COMB.seq.*

40: /cgn2_6/ptodata/1/pna/US6001_COMB.seq.*

41: /cgn2_6/ptodata/1/pna/US6002_COMB.seq.*

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43: /cgn2_6/ptodata/1/pna/US6004_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	21	100.0	21	US-09-423-233-51	Sequence 51, Appl
2	21	100.0	319	US-09-423-233-6	Sequence 6, Appl1
3	19.4	92.4	563	US-09-580-797-10	Sequence 10, Appl
4	19	90.5	561	US-08-905-314-24	Sequence 24, Appl
5	17	81.0	90698	US-09-803-736-1210	Sequence 1210, Ap
6	17	81.0	90698	US-09-803-736-1210	Sequence 1210, Ap
7	17	81.0	141753	US-09-692-412-28	Sequence 28, Appl
8	17	81.0	141753	US-09-803-736-1008	Sequence 1008, Ap
9	16.8	80.0	445	US-09-654-617-4875	Sequence 4875, Ap
10	16.8	80.0	445	US-09-684-016-4875	Sequence 4875, Ap
11	16.2	77.1	313	US-09-205-070-39950	Sequence 39950, A
12	16.2	77.1	313	US-09-321-214-6054	Sequence 6054, A
13	16.2	77.1	313	US-09-340-623-39950	Sequence 39950, A
14	16.2	77.1	313	US-09-516-335-6054	Sequence 6054, Ap
15	16.2	77.1	313	US-09-733-811-6054	Sequence 6054, Ap
16	16.2	77.1	313	US-09-733-811A-6054	Sequence 6054, Ap
17	16.2	77.1	313	US-09-898-888-39950	Sequence 39950, A
18	16.2	77.1	313	US-09-898-888A-39950	Sequence 39950, A
19	16.2	77.1	313	US-09-975-640-6054	Sequence 6054, Ap
20	16.2	77.1	313	US-09-975-640A-6054	Sequence 6054, Ap
21	16.2	77.1	313	US-09-289-768-12122	Sequence 12122, A
22	16.2	77.1	313	US-09-939-397-12122	Sequence 12122, A
23	16.2	77.1	313	US-09-252-833-602	Sequence 602, App
24	16.2	77.1	380	US-09-521-640-55728	Sequence 55728, A
25	16.2	77.1	403	US-09-874-708A-59772	Sequence 59772, A
26	16.2	77.1	403	US-60-211-725-58685	Sequence 58685, A
27	16.2	77.1	427	US-09-293-972-28952	Sequence 28952, A
28	16.2	77.1	427	US-09-904-939-29952	Sequence 29952, A
29	16.2	77.1	474	US-60-360-207-25416	Sequence 25416, A
30	16.2	77.1	489	US-09-606-977-60445	Sequence 60445, A
31	16.2	77.1	499	US-09-634-306B-136133	Sequence 136133, A

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32 16.2 77.1 499 24 US-09-634-306B-136134 Sequence 136134,
33 16.2 77.1 599 28 US-09-702-134-38705 Sequence 38705, A
c 34 16.2 77.1 599 31 US-09-815-264-100800 Sequence 100800,
35 16.2 77.1 745 56 US-60-172-362-3540 Sequence 3540, Ap
36 16.2 77.1 1037 24 US-09-634-306B-259445 Sequence 259445,
37 16.2 77.1 1037 24 US-09-634-306B-259446 Sequence 259446,
38 16.2 77.1 1037 24 US-09-634-306B-259447 Sequence 259447,
39 16.2 77.1 1234 25 US-09-652-125A-9371 Sequence 9371, Ap
40 16.2 77.1 1237 19 US-09-522-303-1121 Sequence 1121, Ap
41 16.2 77.1 1493 24 US-09-620-392-1714 Sequence 1714, Ap
42 16.2 77.1 4005 64 US-60-238-273-238 Sequence 238, Ap
43 16.2 77.1 4343 24 US-09-620-392-17241 Sequence 17241, A
44 16.2 77.1 12260 24 US-09-620-392-17242 Sequence 17242, A
45 16.2 77.1 12792 62 US-60-230-435-71 Sequence 71, Appl
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ALIGNMENTS

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RESULT 1
US-09-423-233-51
; Sequence 51, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-51
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Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ctacacctgcgaactggaga 21
Db 1 ctacacctgcgaactggaga 21

RESULT 2
US-09-423-233-6
; Sequence 6, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6
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Query Match 100.0%; Score 21; DB 18; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 ctacacctgcgaactggaga 21
Db 222 ctacacctgcgaactggaga 242
```

```
RESULT 3
US-09-580-797-10
; Sequence 10, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; APPLICANT: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; TITLE OF INVENTION: Detection of Clinically Relevant Pathogenic Fungal Species
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Fusarium solani
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: n = a or c or g or t
US-09-580-797-10
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Query Match 92.4%; Score 19.4; DB 22; Length 563;
Best Local Similarity 93.2%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 ctacacctgcgaactggaga 21
Db 478 ctacacctgcgaactggaga 498
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```
RESULT 4
US-08-905-314-24
; Sequence 24, Application US/08905314
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novartis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CCC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit"
;
; OTHER INFORMATION: rRNA gene"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..181
; OTHER INFORMATION: /note="ITS 1"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 182..338
; OTHER INFORMATION: /note="5.8S rRNA gene"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 339..504
; OTHER INFORMATION: /note="ITS 2"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 505..561
; OTHER INFORMATION: /note="5' end of large subunit"
;
; OTHER INFORMATION: rRNA gene"
;
US-08-905-314-24
```

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Query Match          90.5%; Score 19; DB 13; Length 561;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 ctacactcgcaactgga 19
    |||||||
DB 445 CTACACTCGCACTGGA 463
```

```

RESULT 5
US-09-803-736-1210
; Sequence 1210, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
;
; SEQ ID NO 1210
; LENGTH: 90698
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
;
US-09-803-736-1210
```

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Query Match          81.0%; Score 17; DB 31; Length 90698;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 cactcgcaactgaga 21
    |||||||
DB 77736 cactcgcaactgaga 77752
```

```

RESULT 6
US-09-803-736-1210/c
; Sequence 1210, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 31
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
;
; SEQ ID NO 1210
; LENGTH: 90698
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
;
US-09-803-736-1210
```

```

Query Match          81.0%; Score 17; DB 31; Length 90698;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 5 cactcgcaactgaga 21
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DB 88914 CACTCGCACTGAGA 88898
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```

RESULT 7
US-09-692-412-28
; Sequence 28, Application US/09692412
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)C
; CURRENT APPLICATION NUMBER: US/09/692,412
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 124
;
; SEQ ID NO 28
; LENGTH: 141753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(141753)
; OTHER INFORMATION: unsure at all n locations
;
US-09-692-412-28
```

```

Query Match          81.0%; Score 17; DB 27; Length 141753;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 cactcgcaactgaga 21
    |||||||
DB 138449 cactcgcaactgaga 138465
```

```

RESULT 8
US-09-803-736-1008
; Sequence 1008, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
```

```
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-11
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1008
; LENGTH: 141753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(141753)
; OTHER INFORMATION: unsure at all n locations
US-09-803-736-1008
```

```
Query Match          81.0%; Score 17; DB 31; Length 141753;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      5 caccctgcgaactggaga 21
Db 138449 caccctgcgaactggaga 138465
```

```
RESULT      9
US-09-654-617-4875
; Sequence 4875, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 4875
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Glycine max
US-09-654-617-4875
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Query Match          80.0%; Score 16.8; DB 25; Length 445;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY      2 taacacctgcgaactggaga 21
Db      1 taacacctgcgaactggaga 20
```

```
RESULT     10
US-09-684-016-4875
; Sequence 4875, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 4875
; LENGTH: 445
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; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-4875
```

```
Query Match          80.0%; Score 16.8; DB 27; Length 445;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 taacacctgcgaactggaga 21
Db      1 taacacctgcgaactggaga 20
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```
RESULT     11
US-09-205-070-39950
; Sequence 39950, Application US/09205070
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748
; CURRENT APPLICATION NUMBER: US/09/205,070
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39950
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(313)
; OTHER INFORMATION: n = A,T,C or G
US-09-205-070-39950
```

```
Query Match          77.1%; Score 16.2; DB 16; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 ctaacacctgcgaactggaga 21
Db      49 ctaacacctgcgaactggaga 69
```

```
RESULT     12
US-09-321-214-6054
; Sequence 6054, Application US/09321214
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Ford, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-740
; CURRENT APPLICATION NUMBER: US/09/321,214
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 60/088,041
; EARLIER FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6054
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-321-214-6054
```



```
Query Match      77.1%; Score 16.2; DB 17; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactggaga 21
      ||||| ||||| | ||||| |||
Db      49 ctactctctcccaactggaga 69

RESULT 13
US-09-340-623-39950
; Sequence 39950, Application US/09340623
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/340,623
; CURRENT FILING DATE: 1999-06-28
; EARLIER APPLICATION NUMBER: US 09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39950
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(313)
; OTHER INFORMATION: n = A,T,C or G
US-09-340-623-39950

Query Match      77.1%; Score 16.2; DB 17; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactggaga 21
      ||||| ||||| | ||||| |||
Db      49 ctactctctcccaactggaga 69

RESULT 14
US-09-516-335-6054
; Sequence 6054, Application US/09516335
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroja, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Palencia, Servando
```

```
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/516,335
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6054
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-516-335-6054

Query Match      77.1%; Score 16.2; DB 19; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 ctacacctgcgaactggaga 21
      ||||| ||||| | ||||| |||
Db      49 ctactctctcccaactggaga 69

RESULT 15
US-09-733-811-6054
; Sequence 6054, Application US/09733811
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroja, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

;; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;; FILE REFERENCE: 740CIP
;; CURRENT APPLICATION NUMBER: US/09/733,811
;; CURRENT FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 09/321,214
;; PRIOR FILING DATE: 1999-05-26
;; PRIOR APPLICATION NUMBER: 60/088,041
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 31906
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6054
;; LENGTH: 313
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-733-811-6054

Query Match 77.1%; Score 16.2; DB 29; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 49 ctactcctcccccaactggaga 69

Search completed: August 22, 2002, 00:39:53
Job time: 13078 sec

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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:57 ; Search time 663.62 seconds
(without alignments)
85.144 Million cell updates/sec

Title: US-10-046-955-51

Sequence: 1 ctacacctgcgaactgaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 172111 seqs, 145317543 residues

Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-10-046-955-51	Sequence 51, Appl
2	21	100.0	319	US-10-046-955-6	Sequence 2637, A
3	17	81.0	510	US-09-620-393B-5270	Sequence 5270, Ap
4	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
5	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
6	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
7	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
8	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,
9	16.2	77.1	33769	PCT-US02-15982-8	Sequence 8, Appl
10	16.2	77.1	33769	US-09-544-398A-8	Sequence 8, Appl
11	16.2	77.1	33769	US-09-544-398B-8	Sequence 8, Appl
12	15.8	75.2	341	US-09-360-039-29617	Sequence 29617, A
13	15.2	72.4	294	US-09-540-210B-34637	Sequence 34637, A
14	15.2	72.4	598	US-10-027-632-22405	Sequence 22405,
15	15.2	72.4	792	US-10-027-632-20739	Sequence 20739, A
16	15.2	72.4	792	US-10-027-632-137644	Sequence 137644,
17	15.2	72.4	792	US-10-027-632-137645	Sequence 137645,
18	15.2	72.4	856	US-10-155-881-37126	Sequence 37126, A
19	15.2	72.4	884	US-10-098-754-14341	Sequence 14341, A
20	15.2	72.4	1244	US-09-886-492-14875	Sequence 14875, A
21	15.2	72.4	1932	US-09-665-308B-17	Sequence 17, Appl
22	15.2	72.4	2685	US-09-835-625-16439	Sequence 16439, A
23	15.2	72.4	2685	US-09-835-625-24778	Sequence 24778, A
24	15.2	72.4	2712	US-09-835-625-9769	Sequence 9769, Ap
25	15.2	72.4	2712	US-09-835-625-26473	Sequence 26473, A

26	15.2	72.4	2757	5	US-09-935-625-10050	Sequence 10050, A
27	15.2	72.4	2757	5	US-09-935-625-26637	Sequence 26637, A
28	15.2	72.4	11485	6	US-10-205-219-144	Sequence 144, Ap
29	14.8	70.5	209	5	US-09-886-492-7487	Sequence 7487, Ap
30	14.8	70.5	258	5	US-09-975-254-27963	Sequence 27963, A
31	14.8	70.5	284	5	US-09-540-210B-34924	Sequence 34924, A
32	14.8	70.5	316	5	US-09-698-495-425	Sequence 425, Ap
33	14.8	70.5	332	5	US-09-886-492-3043	Sequence 3043, Ap
34	14.8	70.5	422	5	US-10-011-154-1257	Sequence 3257, Ap
35	14.8	70.5	478	5	US-09-918-995-11316	Sequence 31316, A
36	14.8	70.5	571	7	US-10-027-632-22591	Sequence 22591, A
37	14.8	70.5	571	7	US-10-027-632-22592	Sequence 22592, A
38	14.8	70.5	571	7	US-10-027-632-22593	Sequence 22593, A
39	14.8	70.5	586	5	US-09-886-492-15318	Sequence 15318, A
40	14.8	70.5	800	7	US-10-027-632-170361	Sequence 170361, A
41	14.8	70.5	906	6	US-10-098-754-11987	Sequence 11987, A
42	14.8	70.5	1161	7	US-10-155-881-35934	Sequence 35934, A
43	14.8	70.5	1155	7	US-10-155-881-35795	Sequence 35795, A
44	14.8	70.5	1214	7	US-10-155-881-14652	Sequence 14652, A
45	14.8	70.5	1372	7	US-10-155-881-14650	Sequence 14650, A

ALIGNMENTS

RESULT 1
US-10-046-955-51
Sequence 51, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 21
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-51

Query Match 100.0% Score 21: DB 7: Length 21:
Best Local Similarity 100.0% Pred. No. 0.15:
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctacacctgcgaactgaga 21
DB 1 ctacacctgcgaactgaga 21

RESULT 2
US-10-046-955-6
Sequence 6, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.

```
APPLICANT: Reiss, Erol
APPLICANT: Aldorevich, Liliانا
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-6
```

```
Query Match          100.0%; Score 21; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 ctacacctcgcaactgaga 21
    ||||| ||||| ||||| |||||
DB 222 ctacacctcgcaactgaga 242
```

```
RESULT 3
US-09-620-393B-5270
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1068P
CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5270
LENGTH: 510
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..510
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..510
OTHER INFORMATION: Ceres Seq. ID 1390380
US-09-620-393B-5270
```

```
Query Match          81.0%; Score 17; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 caccctgcactgaga 21
    ||||| ||||| ||||| |||||
DB 37 caccctgcactgaga 53
```

```
RESULT 4
US-10-027-632-136133
Sequence 136133, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
```

```
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 136133
LENGTH: 499
TYPE: DNA
ORGANISM: Human
US-10-027-632-136133
```

```
Query Match          77.1%; Score 16.2; DB 7; Length 499;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 ctacacctcgcaactgaga 21
    ||||| ||||| ||||| |||||
DB 55 ctacacctcgcaactgaga 75
```

```
RESULT 5
US-10-027-632-136134
Sequence 136134, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 136134
LENGTH: 499
TYPE: DNA
ORGANISM: Human
US-10-027-632-136134
```

```
Query Match          77.1%; Score 16.2; DB 7; Length 499;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 1 ctacacctcgcaactgaga 21
||||| ||||| ||||| |||||
Db 55 ctactcctcccccactgaga 75

RESULT 6
US-10-027-632-259445

; Sequence 259445, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259445
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259445

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
||||| ||||| ||||| |||||
Db 496 ctacccctgcaactgaga 516

RESULT 7
US-10-027-632-259446

; Sequence 259446, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259446
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259446

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
||||| ||||| ||||| |||||
Db 496 ctacccctgcaactgaga 516

RESULT 8
US-10-027-632-259447

; Sequence 259447, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259447
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259447

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
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Db 496 ctacccctgcaactgaga 516

RESULT 9
PCT-US02-15982-8

; Sequence 8, Application PC/TUS0215982
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Yaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 03796-132
; CURRENT APPLICATION NUMBER: PCT/US02/15982
; CURRENT FILING DATE: 2002-05-17

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; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
PCT-US02-15982-8

Query Match      77.1%; Score 16.2; DB 1; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ctaacacctgcgaactggaga 21
      ||| ||||| ||||| |||

Db 25831 ctacgacctctcaactggagaca 25851

RESULT 10
; Sequence 8, Application US/09544398A
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-544-398A-8

Query Match      77.1%; Score 16.2; DB 5; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ctaacacctgcgaactggaga 21
      ||| ||||| ||||| |||

Db 25831 ctacgacctctcaactggagaca 25851

RESULT 11
; Sequence 8, Application US/09544398B
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.

; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are u
US-09-544-398B-8

Query Match      75.2%; Score 15.8; DB 8; Length 341;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 aacacctgcgaactggaga 21
      ||||| ||||| ||||| |||

Db      71 AACACCTTGCAACTGGAAA 53

RESULT 13
; Sequence 34637, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
```

APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/803,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35634
SOFTWARE: PERL Program
SEQ ID NO 34637
LENGTH: 294
TYPE: DNA
ORGANISM: Rattus norvegicus
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: rat00084384
US-09-540-210B-34637

Query Match 72.4%; Score 15.2; DB 5; Length 294;
Best Local Similarity 85.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 taacacctgcgaactgaga 21
|| ||||| || |||||
Db 17 tatcaactcccaactgaga 36

RESULT 14
US-10-027-632-224405
; Sequence 224405, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224405
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-224405

Query Match 72.4%: Score 15.2; DB 7; Length 598;
Best Local Similarity 85.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgag 20
||| ||||| |||||
Db 7 ctacacctcgcaactgag 26

RESULT 15

US-10-027-632-20739
Sequence 20739, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20739

LENGTH: 723

TYPE: DNA

ORGANISM: Human

US-10-027-632-20739

Query Match 72.4%: Score 15.2; DB 7; Length 723;
Best Local Similarity 85.0%: Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgag 20
||| ||||| |||||
Db 646 ctgacacctggaatgag 665

Search completed: August 22, 2002, 00:51:01
Job time: 11901 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:26 ; Search time 8184.59 Seconds

(Without alignments)
843.235 Million cell updates/sec

Title: US-10-046-955-6

319

Sequence: 1 gaaacgcataagtaatgt.....ggataccgcctgaacttaa 319

Scoring table:

IDENTITY_NIC

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Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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40: /cgn2_6/ptodata/1/pna/US6002.COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	319	100.0	319	US-09-423-233-6	Sequence 6, App1
2	241.4	75.7	563	US-09-580-797-10	Sequence 10, App1
3	240.4	75.4	534	US-09-961-755A-7	Sequence 7, App1
4	240.2	75.3	310	US-09-423-233-7	Sequence 7, App1
5	240	75.2	561	US-08-905-314-24	Sequence 24, App1
6	231.4	72.5	637	US-09-580-797-12	Sequence 12, App1
7	187	58.6	504	US-08-905-314-19	Sequence 28, App1
8	183.8	57.6	504	US-08-905-314-19	Sequence 19, App1
9	183.2	57.4	522	US-09-961-755A-5	Sequence 5, App1
10	183.2	57.4	522	US-09-961-755A-8	Sequence 8, App1
11	180.4	56.6	545	US-08-905-314-21	Sequence 21, App1
12	180	56.4	546	US-08-905-314-22	Sequence 22, App1
13	176.4	55.3	521	US-08-961-755A-6	Sequence 6, App1
14	174.8	54.8	503	US-08-905-314-20	Sequence 20, App1
15	171.4	53.7	504	US-09-481-293-32	Sequence 32, App1
16	167	52.4	620	US-09-580-797-11	Sequence 11, App1
17	156.8	49.6	611	PCT-US98-25210-4	Sequence 4, App1
18	145.6	45.2	608	PCT-US98-25210-3	Sequence 3, App1
19	134.2	42.1	382	US-09-241-427-3	Sequence 3, App1
20	128.4	40.3	605	PCT-US98-25210-1	Sequence 1, App1
21	126.6	39.7	365	US-09-423-233-3	Sequence 3, App1
22	125.8	39.4	617	PCT-US98-25210-2	Sequence 2, App1
23	123.2	38.6	365	US-09-423-233-5	Sequence 5, App1
24	122.6	38.4	599	US-09-580-797-37	Sequence 37, App1
25	121.2	38.0	364	US-09-423-233-2	Sequence 2, App1
26	118.6	37.2	608	US-09-580-797-38	Sequence 38, App1
27	118	37.0	568	PCT-US98-25210-5	Sequence 5, App1
28	117.8	36.9	7997	US-60-082-300-11599	Sequence 11599, A
29	117	36.7	727	US-09-580-797-29	Sequence 29, App1
30	116.2	36.4	597	US-09-580-797-35	Sequence 35, App1
31	115.8	36.3	551	US-60-132-861-9331	Sequence 9331, Ap


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OY      2  aaaaatgcgataagtaatgtatgtcaatttcgaataatcatatgatactatcgaattcttgaagcgaac  61
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Db      228  aaaaatgcgataaagtaatgtatgtcaaatcgaatgatcatcgaattcttgaagcgaac  287
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OY      62  attgcgcccgcagatattctgcgagcaltgcctgttcgagcgatcaltcaaacccctcgaagc  121
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Db      288  attgcgcccgcagatattctgcgagcaltgcctgttcgagcgatcaltcaaacccctcgaagc  347
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OY      122  cccgcgcttcggtcggtggatcggcggaagccccctgcgagcgacaagccgctcccca  181
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OY      182  atacgtgacggtcccgccgcagccttccatgtcgtagtagctaacacctgcgaactggag  241
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Db      401  atctatgtggtgcgtctccgcgtcgcacttccatcttgtagtagtaaaacccctgcgaactgtta  460
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OY      242  agcgagcgagccacgacgcgtaaacaacccaactctcgaatgtttgacctcgaatcgaagttag  301
        |||||||
Db      461  cgcgagcgagccacgaagcgtlaaaccccccaacttctgaatgtttgacctcgaatcgaagttag  520
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OY      302  aataccgcgtgaac  315
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Db      521  aataccgcgtgaac  534

RESULT 4
US-09-423-233-7
: Sequence 7, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: Other Filamentous Fungi
: CURRENT APPLICATION NUMBER: US/09/423.233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 310
: TYPE: DNA
: ORGANISM: Fusarium moniliforme
US-09-423-233-7

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[illegible]

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1 RESULT      5
2 US-08-905-314-24
3 ; Sequence 24, Application US/08905314
4 ; GENERAL INFORMATION:
5 ; APPLICANT: Beck, James J.
6 ; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
7 ; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
8 ; NUMBER OF SEQUENCES: 24
9 ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: Novartis Corporation Patent Department
11 ; STREET: 3054 Cornwallis Road
12 ; CITY: Research Triangle Park
13 ; STATE: NC
14 ; COUNTRY: USA
15 ; ZIP: 20779-2257
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: IBM PC compatible
19 ; OPERATING SYSTEM: PC-DOS/MS-DOS
20 ; SOFTWARE: Patent Release #1.0, Version #1.30
21 ; CURRENT APPLICATION DATA:
22 ; APPLICATION NUMBER: US/08/905,314
23 ; FILING DATE:
24 ; CLASSIFICATION: 435
25 ; ATTORNEY/AGENT INFORMATION:
26 ; NAME: Meigs, J. Timothy
27 ; REGISTRATION NUMBER: 38,241
28 ; REFERENCE/DOCKET NUMBER: CGC 1944
29 ; TELECOMMUNICATION INFORMATION:
30 ; TELEPHONE: (919) 541-8587
31 ; TELEFAX: (919) 541-8689
32 ; INFORMATION FOR SEQ ID NO: 24:
33 ; SEQUENCE CHARACTERISTICS:
34 ; LENGTH: 561 base pairs
35 ; TYPE: nucleic acid
36 ; STRANDEDNESS: single
37 ; TOPOLOGY: linear
38 ; MOLECULE TYPE: DNA (genomic)
39 ; ORIGINAL SOURCE:
40 ; STRAIN: Fusarium avenaceum
41 ; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
42 ; FEATURE:
43 ; NAME/KEY: misc_feature
44 ; LOCATION: 1..30
45 ; OTHER INFORMATION: /note="3' end of small subunit
46 ; OTHER INFORMATION: rRNA gene"
47 ; FEATURE:
48 ; NAME/KEY: misc_feature
49 ; LOCATION: 31..181
50 ; OTHER INFORMATION: /note="ITS 1"
51 ; FEATURE:
52 ; NAME/KEY: misc_feature
53 ; LOCATION: 182..338
54 ; OTHER INFORMATION: /note="5.8S rRNA gene"
55 ; FEATURE:
56 ; NAME/KEY: misc_feature
57 ; LOCATION: 339..504
58 ; OTHER INFORMATION: /note="ITS 2"
59 ; FEATURE:
60 ; NAME/KEY: misc_feature
61 ; LOCATION: 505..561
62 ; OTHER INFORMATION: /note="5' end of large subunit
63 ; OTHER INFORMATION: rRNA gene"
64 US-08-905-314-24

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	Query Match	Score	DB	Length
Best Local Similarity	88.7%	Pred. NM.1.1e-67		
Matches	282	2	Mismatches	7
			Indels	2
			Gaps	2


```

:
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 504 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORGANISM: Fusarium culmorum
: INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
: INDIVIDUAL ISOLATE: (consensus sequence)
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..12
: OTHER INFORMATION: /note="3' end of small subunit"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 13..161
: OTHER INFORMATION: /note="ITS 1"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 162..318
: OTHER INFORMATION: /note="5.8S rRNA gene"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 319..472
: OTHER INFORMATION: /note="ITS 2"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 473..504
: OTHER INFORMATION: /note="5' end of large subunit"
:
: OTHER INFORMATION: rRNA gene"
:
US-08-905-314-19

Query Match          57.6%; Score 183.8; DB 13; Length 504;
Best Local Similarity 81.5%; Pred. No. 5,7e-44;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

Oy 2 aaaaatgcgataagtaattgcaatgcagaatcagtaaatcgaatccttgaacgac 61
    |||
Db 211 AAAATGCGATAGTAATGTAATGCAATTCAGATGATCATGAACTTTGAACGCAC 270

Oy 62 attgcgcgcgcagatctctgacggcgacatgcttcgagcgatcattacaacccctcaggc 121
    |||
Db 271 ATTGCGCGCGCAGATATTCTGGCGGCATGCTGTGACGCGTCATTTCACCCCTCAAGC 330

Oy 122 ccccgagcctgagtggtggagatcgcgaggaagccccctcgcgagcaaacgcccgtcccca 181
    |||
Db 331 CC---AGCTTGTTGTTGGAGACTG-----CAGTCCTGCTGCACCTCCCAA 372

Oy 182 atacagtgagcggtccgcagcgagcttcagtgcgtagtagtaaacactcgaactcagag 241
    |||
Db 373 ATACATTGCGCGTACGTCGRAGCTTCATAGCGTAGTAATTATCATATGCTTACTGTA 432

Oy 242 agcgagcgagcgacgcccataaacaccaacttcgaatgltgagcctcgaatcagaglag 301
    |||
Db 433 ATCGTCGGCGGCTACGCGCTTAAC-CCCAACTTCTGAATGTGACCTCGGATCAGTAGG 491

Oy 302 aataccgcgtgaa 314
    |||
Db 492 AATACCCGCTGAA 504

RESULT 9
US-09-961-755A-5
; Sequence 5, Application US/09961755A
```

```

:
: GENERAL INFORMATION:
: APPLICANT: Beck, Jim
: TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
: FILE REFERENCE: 60055
: CURRENT APPLICATION NUMBER: US/09/961,755A
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 522
: TYPE: DNA
: ORGANISM: Fusarium subglutinans
:
US-09-961-755A-5

Query Match          57.4%; Score 183.2; DB 36; Length 522;
Best Local Similarity 83.4%; Pred. No. 8,7e-44;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Oy 2 aaaaatgcgataagtaattgcaatgcagaatcagtaaatcgaatccttgaacgac 61
    |||
Db 228 aaaaatgcgataagtaattgcaatgcagaatcagtaaatcgaatccttgaacgac 287

Oy 62 attgcgcgcgcagatctctgacggcgacatgcttcgagcgatcattacaacccctcaggc 121
    |||
Db 288 attgcgcgcgcagatctctgacggcgacatgcttcgagcgatcattacaacccctcaggc 347

Oy 122 ccccgagcctgagtggtggagatcgcgaggaagccccctcgcgagcaaacgcccgtcccca 181
    |||
Db 348 CC---agcttggtggtggagctc-----ggagtcgaatcgcgtcccca 390

Oy 182 atacagtgagcggtccgcagcgagcttcgaatcgtgtagtagtaaacctcgaactcagag 241
    |||
Db 391 atgattgagcgatcagctg-agcttcgaatcgtgtagtagtaaacctcgaactcagag 449

Oy 242 agcgagcgagcgacgcccataaacaccaacttcgaatgltgagcctcgaatcagaglag 301
    |||
Db 450 atcgtcgagcgacgcccgttaaac-cccaacttcgaatgltgagcctcgaatcagaglag 508

Oy 302 aataccgcgtgaa 315
    |||
Db 509 aataccgcgtgaa 522

RESULT 10
US-09-961-755A-8
; Sequence 8, Application US/09961755A
: GENERAL INFORMATION:
: APPLICANT: Beck, Jim
: TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
: FILE REFERENCE: 60055
: CURRENT APPLICATION NUMBER: US/09/961,755A
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 8
: LENGTH: 522
: TYPE: DNA
: ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
:
US-09-961-755A-8

Query Match          57.4%; Score 183.2; DB 36; Length 522;
Best Local Similarity 83.4%; Pred. No. 8,7e-44;
Matches 262; Conservative 0; Mismatches 33; Indels 19; Gaps 4;

Oy 2 aaaaatgcgataagtaattgcaatgcagaatcagtaaatcgaatccttgaacgac 61
    |||
Db 228 aaaaatgcgataagtaattgcaatgcagaatcagtaaatcgaatccttgaacgac 287
```

```

OY 62 atgcgcccagcagatctctgagggagcagtcgcttcgagcgatcaaccctcagc 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 atgcgcccagcagatctctgagggagcagtcgcttcgagcgatcaaccctcagc 347
OY 122 ccccgagcctgctggtggagtcgcgcgaagcccccctgcggcacaacgcgtccccc 181
    || || || || || || || || || || || || || || || || || || || ||
Db 348 ccc---agctcgtgcttgggagctc-----gcgagtcgaatcgcttccccc 390
OY 182 atacagtgagcgtccgcgcagcctccatcttgctgtagtgcgtaacacccctcgaactgag 241
    || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 atgattgagcgtgcaacgtcg-agctccatagcgtagtagtaaacaccctcgttaactgta 449
OY 242 agcgagcgagcgcagcgcgtlaaaacacccaactctgtaatgltgacctcgatcaagtagag 301
    || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 450 atcgtcgcgcgcacgcgcgtlaaac-cccactctgtaatgltgacctcgatcaagtagag 508
OY 302 aataccgcgtgaac 315
Db 509 aataccgcgtgaac 522

```

```

RESULT 11
: Sequence 21. Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 545 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Fusarium moniliforme
: INDIVIDUAL ISOLATE: 4551
: IMMEDIATE SOURCE:
: CLONE: pCRMON1
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note="3' end of small subunit
: FEATURE:
: NAME/KEY: misc_gene
: LOCATION: 31..178

```

```

: OTHER INFORMATION: /note="ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 179..335
: OTHER INFORMATION: /note="5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 336..488
: OTHER INFORMATION: /note="ITS 2"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 489..545
: OTHER INFORMATION: /note="5' end of large subunit
: OTHER INFORMATION: rRNA gene"
: US-08-905-314-21

```

```

Query Match      56.6%; Score 180.4; DB 13; Length 545;
Best Local Similarity 82.4%; Pred. No. 6e-43;
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

```

```

OY 2 aaaaatgcataatgaatgtaattgcagaatcagtgatcaatcgaatccttgaagcac 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 AAAATGCGATAGTAATGTGAATTGCAAAATTCAGTGAATCATCGAATCTTGAACGCAC 287
OY 62 atgcgcccagcagatctctgagggagcagtcgcttcgagcgatcaaccctcagc 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 ATGCGCCCGCAGTATCTTGGCGGCGATGCTTTGAGCGTATTTCAACCTCAAGC 347
OY 122 ccccgagcctgctggtggagtcgcgcgaagcccccctgcggcacaacgcgtccccc 181
    || || || || || || || || || || || || || || || || || || || ||
Db 348 CC---AGCTGTGTTGGAGACTG-----CAGTCTCTGCTGCACATCCCA 369
OY 182 atacagtgagcgtccgcgcagcctccatcttgctgtagtgcgtaacacccctcgaactgag 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 390 ATACATTGGCGGTACGTCG-AGCTTCATAGCCTACTTAATTACATCGTTACTGTGA 448
OY 242 agcgagcgagcgcagcgcgtlaaaacacccaactctgtaatgltgacctcgatcaagtagag 301
    || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 ATGTCGGCGGCACGCGCTTAAC-CCCACTTGTGAATGTGACCTCGGATCAGTAGG 507
OY 302 aataccgcgtgaactaa 319
Db 508 AATACCGCTGAACCTTAA 525

```

```

RESULT 12
: Sequence 22. Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241

```



```

: REFERENCE/DOCKET NUMBER: CCC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 546 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Fusarium poae
: INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
: IMMEDIATE SOURCE:
: CLONE: PCRPOAET427(1-2), PCRPOAET534(2-2), and
: PCRPOAET756(3-1)
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note= "3' end of small subunit"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..180
: OTHER INFORMATION: /note= "ITS 1"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 181..337
: OTHER INFORMATION: /note= "5.8S rRNA gene"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 338..489
: OTHER INFORMATION: /note= "ITS 2"
:
: NAME/KEY: misc_feature
: LOCATION: 490..546
: OTHER INFORMATION: /note= "5' end of large subunit"
:
: OTHER INFORMATION: rRNA gene"
:
: US-08-905-314-22

```

```

Query Match          56.4%; Score 180; DB 13; Length 546;
Best Local Similarity 82.4%; Pred. No. 7.9e-43;
Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4;

```

```

OY 2 aaatgagataaataatgtaattgcaagaattcagtaacatcgaactcttgaacgcac 61
   |||||||
DB 230 AAAATGCGATAGTAATGTAATGAGAAATTCAGTGAATCAGTAATCTTTGAACGCAC 289
   |||||||
OY 62 atgagccgcagatattctgagcgagcaltcgttcgagcgtcatcaaacctcagac 121
   |||||||
DB 290 ATTGCGCGCCGCAATATTCTGGCGGAGATCCTGTCGACGTCATTTCAACCTCAAGC 349
   |||||||
OY 122 ccccgagcctgagcttgaggatcgagcggaagccccctgagcgagcaacgcgcctccca 181
   |||||||
DB 350 CC---ACCTTGCTGTGG-----ATCTGTGTGCAAAACACACTCCCAA 390
   |||||||
OY 182 atacagtgagcggtccgcagcttcacgttcagtaagtaacacccctcgaactcagag 241
   |||||||
DB 391 ATTGATTGGGGTGACCTCG-AGCTTCATACGCTAGTAATTACACATGCTTACTGGTA 449
   |||||||
OY 242 agcgagcgagcagcagcagtaaacacccacacttcgaatgltgaactcgaatcagtagg 301
   |||||||
DB 450 ATGCTCGCGGCAAGCGCTTAAAC-CCCAACTTCTGAATGTGACCTCGATCAGTAGG 508
   |||||||
OY 302 aatcccgctgaactaa 319
   |||||||
DB 509 AATACCGCTGAACCTTAA 526

```

RESULT 13

```

US-09-961-755A-6
: Sequence 6, Application US/09961755A
: GENERAL INFORMATION:
: APPLICANT: Beck, Jim
: TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
: TITLE OF INVENTION: Polymerase Chain Reaction
: FILE REFERENCE: 60055
: CURRENT APPLICATION NUMBER: US/09/961,755A
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Version 3.0
: SEQ ID NO 6
: LENGTH: 521
: TYPE: DNA
: ORGANISM: Glbberella zeae
:
: US-09-961-755A-6

```

```

Query Match          55.3%; Score 176.4; DB 36; Length 521;
Best Local Similarity 82.2%; Pred. No. 9.2e-42;
Matches 258; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

```

```

OY 2 aaatgagataaataatgtaattgcaagaattcagtaacatcgaactcttgaacgcac 61
   |||||||
DB 228 aaatgagataaataatgtaattgcaagaattcagtaacatcgaactcttgaacgcac 287
   |||||||
OY 62 atgagccgcagatattctgagcgagcaltcgttcgagcgtcatcaaacctcagac 121
   |||||||
DB 288 atgagccgcagatattctgagcgagcaltcgttcgagcgtcatcaaacctcagac 347
   |||||||
OY 122 ccccgagcctgagcttgaggatcgagcggaagccccctgagcgagcaacgcgcctccca 181
   |||||||
DB 348 CC---AGCTTGCTGTGGAGCTG-----CAGTCTGCTGCACTCCCAA 389
   |||||||
OY 182 atacagtgagcggtccgcagcttcacgttcagtaagtaacacccctcgaactcagag 241
   |||||||
DB 390 atacatgagcggtcagctcg-AGCTTCATAGCGTAAGTAATTACACATGCTTACTGGTA 448
   |||||||
OY 242 agcgagcgagcagcagcagtaaacacccacacttcgaatgltgaactcgaatcagtagg 301
   |||||||
DB 449 atcgtcgcgagcagcgagtaaac-cccaacttcgaatgltgacctcgatcagtagg 507
   |||||||
OY 302 aatcccgctgaac 315
   |||||||
DB 508 aatcccgctgaac 521

```

```

RESULT 14
US-08-905-314-20
: Sequence 20, Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257

```

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:

```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:48 ; Search time 663.62 Seconds

(Without alignments)
1293.380 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 1 gaaatgcataagtaatgt.....ggaataccgcgtgaactaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1721111 seqs, 1345317543 residues

Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
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8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	7	US-10-046-955-6
2	240.2	75.3	310	7	US-10-046-955-7
3	131.8	41.3	652	1	PCR-US02-11769-2
4	126.6	39.7	365	7	US-10-046-953-3
5	123.2	38.6	365	7	US-10-046-955-5
6	121.2	38.0	364	7	US-10-046-955-2
7	119.8	37.6	650	1	PCR-US02-11769-4
8	114.2	35.8	641	5	US-09-766-173C-4
9	111.2	34.9	346	7	US-10-046-955-24
10	110.6	34.7	618	5	US-10-046-955-25
11	110.2	34.5	343	7	US-09-766-173C-5
12	110.2	34.5	344	7	US-10-046-955-27
13	109.4	34.3	536	5	US-09-517-790-5
14	109.2	34.2	346	7	US-10-046-955-25
15	108	33.9	309	7	US-10-046-955-28
16	106.4	33.4	336	7	US-10-046-955-29
17	97	30.4	515	5	US-09-517-790-1
18	97	30.4	523	5	US-09-517-790-4
19	96.4	30.2	355	7	US-10-046-955-4
20	93	29.2	516	5	US-09-517-790-2
21	91.4	28.7	570	5	US-09-517-790-3
22	62	19.4	327	7	US-10-046-955-10
23	62	19.4	328	7	US-10-046-955-8
24	62	19.4	330	7	US-10-046-955-8
25	62	19.4	330	7	US-10-046-955-12

26	55.8	17.5	1180	7	US-10-155-881-2120	Sequence 2120, Ap
27	55.6	17.4	322	7	US-10-046-955-11	Sequence 11, Appl
28	55	17.2	2091	5	US-09-935-625-5545	Sequence 5545, Ap
29	55	17.2	2091	5	US-09-935-625-17457	Sequence 17457, A
30	55	17.2	2091	5	US-09-935-625-55992	Sequence 25792, A
31	55	17.2	2091	5	US-09-935-625-55992	Sequence 5599, Ap
32	55	17.2	2097	5	US-09-935-625-6116	Sequence 6116, Ap
33	55	17.2	2097	5	US-09-935-625-17511	Sequence 17511, A
34	55	17.2	2097	5	US-09-935-625-18547	Sequence 18547, A
35	55	17.2	2097	5	US-09-935-625-25913	Sequence 25913, A
36	55	17.2	2097	5	US-09-935-625-26950	Sequence 26950, A
37	55	17.2	4310	7	US-10-177-253-71	Sequence 71, Appl
38	54.6	17.1	131	5	US-09-975-254-5041	Sequence 5041, Ap
39	54.6	17.1	250	5	US-09-975-254-4556	Sequence 4556, Ap
40	54.6	17.1	1414	7	US-10-155-881-6537	Sequence 6537, Ap
41	54.6	17.1	3927	7	US-10-155-881-16180	Sequence 16180, A
42	54	16.9	486	7	US-10-046-955-19	Sequence 19, Appl
43	52.6	16.5	1037	7	US-10-155-881-2313	Sequence 2313, Ap
44	52.6	16.5	3460	8	US-60-391-781-202	Sequence 202, App
45	52.4	16.4	949	7	US-10-155-881-3328	Sequence 3328, Ap

ALIGNMENTS

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RESULT 1
US-10-046-955-6
: Sequence 6, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 319
: TYPE: DNA
: ORGANISM: Fusarium solani
: US-10-046-955-6
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Query Match 100.0% Score 319; DB 7; Length 319;
Best Local Similarity 100.0% Pred. No. 6e+84;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 gaaatgcataagtaatgtgaattcagatcagaattcagtaacatcagaattccttgaagca 60
DB 1 gaaatgcataagtaatgtgaattcagatcagaattcagtaacatcagaattccttgaagca 60
QY 61 catggccgcgcgaattatcttggcggaatgcgcgtcttgagcgtcattacaaccctcagg 120
DB 61 catggccgcgcgaattatcttggcggaatgcgcgtcttggagcgtcattacaaccctcagg 120
QY 121 ccccccggccttgctgggagtcgagcgaagcccccgcggaacgaacgcgcgtcccca 180
DB 121 ccccccggccttgctgggagtcgagcgaagcccccgcggaacgaacgcgcgtcccca 180
QY 181 aatacagtgaggcgtccgcgcgaagcttcacattcgtagtagtaacacccctgcgaattga 240
```



```

; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-046-955-3

```

Query Match	39.7%	Score 126.6;	DB 7;	Length 365;
Best Local Similarity	64.7%	Pred. No. 1.7e-27;		
Matches 205; Conservative	0;	Mismatches 109;	Indels 3;	Gaps 1;

[illegible]

```

RESULT      5
US-10-046-955-5
: Sequence 5, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423, 233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
: US-10-046-955-5

```

Query Match	38.68;	Score 123.2;	DB 7;	Length 365;
Best Local Similarity	66.08;	Pred. No. 1,76-26;		
Matches 210; Conservative	0;	Mismatches 103;	Indels 5;	Gaps 2;

[illegible]

```

RESULT 6
; Sequence 2, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: Other Filamentous Fungi
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
; US-10-046-955-2

```

Query Match	38.0%;	Score 121.2;	DB 7;	Length 364;
Best Local Similarity	65.9%;	Pred. No. 6.7e-26;		
Matches 211;	Conservative	0;	Mismatches 98;	Indels 11;
			Gaps 2;	
QY	3	aatgcgataagtaatggaattgcagaattgaagatcatcgatctttgaagcaca	62	
DB	52	aaatgcgataaactaatgtaattgcagaattgaatgatacatcgatctttgaagcaca	111	
QY	63	ttagcccccgcgataattctcgcgaggcagatccctgttcgagcgatcataacaacctgaagcc	122	
DB	112	ttagcccccgcgataattctcgcgaggcagatccctgttcgagcgatcataacaacctgaagcc	171	
QY	123	cccgagcctgagcgtttggggatcgcgcgaaagccccctgcgagcagacaaagcgcgtcccccana	182	
DB	172	acggatcttgatatttgagccccgcgattccccctctcccgag-----aacggagcccgana	223	

```
OY 183 tacagtgagcgtccgcgcgcagcttcacatctgctagtagtaaacacctcgcgaactgagga 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 ggcagcggcgagccgcgcgtccgcgcgtacgagcgtatggcgcttcgacactcgtcgtag 283
OY 243 gcgcgcgcgcgcgcgcgcgcgttaaacaccc---aacctctaatgctgcgaactcagta 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 ccgcgcgcgcgcgcgcgcgcacacacacattatcttctaaagtgtgacactcgatcagta 343
OY 300 ggaataccgcgtgaactaa 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 ggagataccgcgcgtgaactaa 363
```

RESULT 7

PCT-US02-11769-4

Sequence 4, Application PC/TUS0211769

```
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AO 2019, 40
; CURRENT APPLICATION NUMBER: PCT/US02/11769
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Muscador roseus
PCT-US02-11769-4
```

```
Query Match 37.6%; Score 119.8; DB 1; Length 650;
Best Local Similarity 72.2%; Pred. No. 1.9e-25;
Matches 229; Conservative 0; Mismatches 72; Indels 16; Gaps 5;
```

```
OY 3 aatgcgataagtaatgtaattgtaataatcagtgatctcgaatcttgaacgcaca 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 aatgcgataagtaatgtaattgtaataatcagtgatctcgaatcttgaacgcaca 388
OY 63 ttgcgcgcgcgcgcgcgcgcgcgtctgctgagcgtcttcaaaccccgagcc 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 ttgcgcgcgcgcgcgcgcgcgcgtctgagcgtcttcaaaccccgagcc 447
OY 123 ccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 ctgtgcttaagcgttggagcgtctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 495
OY 183 tacagtgagcgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 486 gtgattgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 553
OY 243 gcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 ggttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 612
OY 303 ataccgcgtgaactaa 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 ataccgcgtgaactaa 629
```

RESULT 8

US-09-766-173C-4

Sequence 4, Application US/09766173C

```
; GENERAL INFORMATION:
; APPLICANT: Carroll, George C.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Pathogenic Guignardia Citricarpa
```

```
; FILE REFERENCE: Oregon 99-09
; CURRENT APPLICATION NUMBER: US/09/766,173C
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/177,013
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Guignardia Citricarpa
US-09-766-173C-4
```

```
Query Match 35.8%; Score 114.2; DB 5; Length 641;
Best Local Similarity 62.5%; Pred. No. 8.4e-24;
Matches 198; Conservative 0; Mismatches 113; Indels 6; Gaps 1;
```

```
OY 3 aatgcgataagtaatgtaattgtaataatcagtgatctcgaatcttgaacgcaca 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 aatgcgataagtaatgtaattgtaataatcagtgatctcgaatcttgaacgcaca 377
OY 63 ttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 ttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 437
OY 123 ccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 438 ctgtgcttaagcgttggagcgtctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 491
OY 183 tacagtgagcgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 ccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 551
OY 243 gcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 ccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 611
OY 303 ataccgcgtgaactaa 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 ataccgcgtgaactaa 628
```

RESULT 9

US-10-046-955-24

Sequence 24, Application US/10046955

```
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Erol
; APPLICANT: Aldorevich, Lilliana
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Pseudallescheria boydii
```


Oy	62	atcgcgccgacagtaattctcgcgcggaatccctgttccgaagtcataaacacctaaagg	121
Db	62	atcgcgccgacagtaattctcgcgcggaatccctgttccgaagtcataaacacctaaagg	121
Oy	122	ccccg-----ggccctcgatctggagatccgcggagaagccccttcggag	163
Db	122	ctcgcgttccctcaaggaaagcccaagggtccggtgtttggggcgctaaggaaagtcttcgc	180
Oy	164	cacaagcgcgtccccaataacagttvgcggtcccgccgcgaagcttccat-tgcttagtag-	221
Db	181	ccctccgaagcccttgataatcacgttcggttcccgccgcygtttgcctcttcgtagaagt	240
Oy	222	----ctaacactcgcgaactggaagagggcgcgccgcgaagctaaaacaccgaactctg	277
Db	241	ctctcttgcaagctcgcgatctgggtcccgcgggagcgctgcgcataaacacactataatc	300
Oy	278	aa---tgtgacctgcaatcaggtaggaatacccgctgaacttaa	319
Db	301	caaatggttttacctcgcgataaggtataggtttaaccgcgtgaacttaa	346

```

RESULT 15
US-10-046-955-28
: Sequence 28, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 28
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Penicillium notatum
: US-10-046-955-28

```

Query Match	33.98;	Score 108;	DB 7;	Length 309;
Best Local Similarity	67.58;	Pred. No. 4.9e-22;		
Matches 216; Conservative	0;	Mismatches 90;	Indels 14;	Gaps 4

[illegible][illegible]

Search completed: August 22, 2002, 00:50:49
Job time: 11889 sec

|

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:47 ; Search time 2238.68 Seconds
(without alignments)
2897.791 Million cell updates/sec

Title: US-10-046-955-7
Perfect score: 1 aatgcatgaatgaatga.....ggataccgcgtaactaa 310
Sequence: 310

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_inu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	310	100.0	310	8	AF117922	AF117922 Gibberell
2	306.8	99.0	351	8	AF162903	AF162903 Fusarium
3	306.8	99.0	558	8	FEUJRNA	X94176 Fusarium fu
4	306.8	99.0	558	8	FPORRNA	X94171 Fusarium pr
5	306.8	99.0	569	8	AF452163	AF452163 Pythium u
6	306.8	99.0	596	8	AF291061	AF291061 Fusarium
7	306.8	99.0	2293	6	ARI68094	ARI68094 Sequence
8	305.2	98.5	531	8	AF158303	AF158303 Fusarium
9	305.2	98.5	540	8	AF158304	AF158304 Fusarium
10	303.6	97.9	540	8	AF158302	AF158302 Fusarium
11	302.8	97.7	534	8	FEU34557	U34557 Fusarium fu
12	302.8	97.7	534	8	FEU34558	U34558 Fusarium pr
13	301.2	97.2	534	8	FAU61670	U61670 Fusarium an
14	301.2	97.2	534	8	FSU61693	U61693 Fusarium sp
15	300.8	97.0	502	8	AF165873	AF165873 Gibberell
16	299.6	96.6	534	8	FPURRNA	U34574 Fusarium ph
17	297.2	95.9	559	8	FREDRNA	X94169 Fusarium re
18	296.4	95.6	534	8	FSU34567	U34567 Fusarium sp
19	296.4	95.6	534	8	FSU61692	U61692 Fusarium sp
20	294.8	95.1	534	8	FSU34564	U34564 Fusarium sp
21	294.2	94.9	541	8	AF158307	AF158307 Fusarium
22	294.2	94.9	541	8	AF158309	AF158309 Fusarium
23	294.2	94.9	559	8	FDLARNNA	X94177 Fusarium dl
24	291	93.9	527	8	FSU61687	U61687 Fusarium q1
25	290.8	93.8	521	8	FSU61691	U61691 Fusarium ap
26	290.2	93.6	535	8	FAU34573	U34573 Fusarium ac
27	290	93.5	535	8	FSU34565	U34565 Fusarium re
28	289.2	93.3	522	8	FCU61678	U61678 Fusarium co
29	289	93.2	542	8	AF008920	AF008920 Fusarium
30	288.6	93.1	535	8	FDU34572	U34572 Fusarium dl
31	288.4	93.0	349	8	AF162897	AF162897 Fusarium
32	288.4	93.0	529	8	AF158312	AF158312 Fusarium
33	288.4	93.0	557	8	FNCRRNA	X94174 Fusarium ny
34	284.4	91.7	533	8	FN034568	U34568 Fusarium ny
35	284.4	91.7	533	8	FU034575	U34575 Fusarium ud
36	278.2	89.7	533	8	FBU34581	U34581 Fusarium bu
37	272.4	87.9	532	8	FSU34560	U34560 Fusarium th
38	270.8	87.4	520	8	FSU61690	U61690 Fusarium ap
39	270.8	87.4	1458	8	AF310981	AF310981 Fusarium
40	269.2	86.8	538	8	PPU18954	U18954 Pseudofusar
41	268.4	86.6	538	8	FSU61695	U61695 Fusarium sp
42	267.2	86.2	471	8	AF150468	AF150468 Nectria h
43	267.2	86.2	1460	8	AF310976	AF310976 Fusarium
44	267.2	86.2	1460	8	AF310977	AF310977 Fusarium
45	266.8	86.1	1456	8	AF310982	AF310982 Fusarium

ALIGNMENTS

RESULT 1
AF117922 310 bp DNA linear PLN 17-JUN-2000
LOCUS
DEFINITION Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial
sequence; Internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION
AF117922
VERSION
AF117922.1 GI:8570108
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 310)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Rapid differentiation of filamentous fungi using species-specific
DNA probes
JOURNAL
2 (bases 1 to 310)
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE
AUTHORS
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Direct Submission
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

FEATURES	Location/Qualifiers
source	1..310
	/organism="Gibberella fujikuroi"
	/strain="ATCC 38519"
	/db_xref="ATCC:38519"
	/db_xref="taxon:5127"
rRNA	<1..159
	/product="5.8S ribosomal RNA"
mlsC_RNA	159..272
	/note="ITS2"
rRNA	/product="Internal transcribed spacer 2"
	273..>310
BASE COUNT	/product="28S ribosomal RNA"
ORIGIN	73 a 86 c 80 g 71 t

	Query Match	100.0%; Score 310; DB 8; Length 310;
	Best Local Similarity	100.0%; Pred. No. 4, 6e-85;
	Matches 310; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1	aaalcgataagtaatcgtgaattgcanaaatlcaigtgaalcatcgaalccttgaacgaca 60
Db	1	AAATGCCCATTAAGTAAAGTGAATTGCAAAATTCAGTAATCTATCCAAATCTTTGAACGCACA 60
Oy	61	ttagcccccgcgaatcttcgcggcgacatgcgtttcgcgagcgctaaattccaacctcaaggcc 120
Db	61	TTTGCGCCCCGCAATATTCTGGCGGCGCATGCTGTTCGAGCGTCAATTTCAACCTCAGCC 120
Oy	121	ccccgggttggttggttggtgggatcgcgaagcccttcgcggaagccgcgccgaaactagt 180
Db	121	CCCCGGTTTTGCTTTGGGATGGCGAAGCCCTTTGGCGCAACCSCGCCCAAATCTAGTG 180
Oy	181	ggaggttcggttcgaagttccatttggtgtagtaaaccctcgcgaacttgtlaacggcgcc 240
Db	181	GCGGTCTCGCTGACGACTTCCTCATTTGCGTAGTAATAAACCTTCGCAACTGGTAGCGGCGC 240
Oy	241	ggccaaagccgtlaaaccccccaactctcgaatgtgcacctcgcgatcagtagaataaccg 300
Db	241	GGCCAAACCCCTTTAAACCCCAACTCTGTAATGTTCACCTCGGATCAGGTAGAAATACCG 300
Oy	301	ctgaacctaa 310
Db	301	CTGACTTAA 310
RESULT 2		
AF162903		
LOCUS	Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence,	351 bp DNA linear PLN 04-AUG-1999
DEFINITION	Internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.	
ACCESSION	AF162903	
VERSION	AF162903.1 GI:5690392	
KEYWORDS	.	
SOURCE	Fusarium proliferatum.	
ORGANISM	Fusarium proliferatum.	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex 1 (bases 1 to 351)	
AUTHORS	Min, B.R.	
TITLE	Direct Submission	
JOURNAL	Submitted (28-JUN-1999) BIOLOGY, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea	
FEATURES	Location/Qualifiers	
source	1..351	
	/organism="Fusarium proliferatum"	
	/strain="6787"	
rRNA	/db_xref="taxon:42674"	
	<1..128	
misc_RNA	/product="5.8S ribosomal RNA"	
	129..293	
	/product="internal transcribed spacer 2"	

	294 . .>351	/product="28S ribosomal RNA"
RNA		
BASE COUNT	87 a	94 c 94 g 76 t
ORIGIN		

Query Match	99.08;	Score 306.8;	DB 8;	Length 351;
Best Local Similarity	99.48;	Pred. No. 4.6e-84;		
Matches 308; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

OY	1	aaatcgcgaataagatgaaatcgaataatcagtagatcatcgaatccttgaagcgaca	60
Db	22	AAATGCGAATGAATGATGATTCAGATTCAGATTCATCATCTTGAAATCGACA	81
OY	61	ttgcgcgccgcgaatattctcgcgcgcgcgcgcgtctgttcgaagtcattcaacctcaagcc	120
Db	82	TTGCGCCCGCCAGATATTTGGCGGGCAGTCCCTGTTTCAGAGCTCATTTCAACCCCTCAAGCC	141
OY	121	ccgcggtcttgtagtctgtaggaatcgcgaagcccttcgcgcgaagccgcgcgcgaatctagt	180
Db	142	CCCGGGTTTGATGTTGGGGATCGGGGAGCCCTTGCGGCAAGCCGGCCGGAATCTAGTG	201
OY	181	ggcgatctcgcgcgcgcgttcattcgttagtagtaaaacctcgcgaatctgtgaatcgcgcgc	240
Db	202	GCGGCTCTGCGCAGACTTCATTCAGTAGTAACCCCTCGCAACTGGTATCCCGGGCGC	261
OY	241	ggccaagccggttaaaccgcccaactctcgaatcttgacctcgcgaatcgaatgaataaccg	300
Db	262	GGCCAAGCCGTTAAACCCCAACTTTCGATGTTGACCTCGGATCAGGTAGGAATATCCG	321
OY	301	ctgaacttaa 310	
Db	322	CTGAACCTTAA 331	

FEFURRNA	RESULT	3
LOCUS		
DEFINITION	Fusarium fujikuroi 58 bp DNA linear	PLN 14-JUN-2001
ACCESSION	Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).	
VERSION	X94176.X93900	
KEYWORDS	X94176.1 GI:1122868	
	18S ribosomal RNA: 18S rRNA gene; 28S ribosomal RNA: 28S rRNA gene; 5.8S ribosomal RNA: 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.	
SOURCE	Gibberella fujikuroi.	
ORGANISM	Gibberella fujikuroi	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex	
AUTHORS	1 (bases 1 to 558)	
TITLE	Maalwijk C., de Koning, J. R. A., Baayen, R. P. and Gams, W.	
JOURNAL	Discordant groupings of Fusarium spp. from sections Elegans, Liseola and Diamantina based on ribosomal ITS1 and ITS2 sequences	
REFERENCE	Mycologia 88, 361-368 (1996)	
AUTHORS	2 (bases 1 to 558)	
TITLE	Maalwijk C.	
JOURNAL	Direct Submission	
	Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS	
COMMENT	On Jun 15, 2001 this sequence version replaced g1:1103564. Overlaps with X78260.	
FEATURES	Location/Qualifiers	
source	1..558	
	/organism="Gibberella fujikuroi"	
	/strain="CBS 221.76"	
	/specific_host="rice"	
	/db_xref="taxon:5127"	
RNA	<1..30	
	/gene="18S rRNA"	
	/product="18S ribosomal RNA"	
gene	1..30	
	/gene="18S rRNA"	

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misc_feature 31..177
                /note="Internal transcribed spacer 1, ITS1"
rRNA 178..335
                /gene="5.8 rRNA"
                /product="5.8 ribosomal RNA"
gene 178..335
                /gene="5.8 rRNA"
misc_feature 336..500
                /note="Internal transcribed spacer 2, ITS2"
rRNA 501..558
                /gene="28S rRNA"
                /product="28S ribosomal RNA"
gene 501..558
                /gene="28S rRNA"
BASE COUNT 144 a 152 c 137 g 125 t
ORIGIN
Query Match 99.0%; Score 306.8; DB 8; Length 558;
Best Local Similarity 99.4%; Pred. No. 4.9e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaatgcataagtaatgtaattgcaaatctcagtaatcatcgaatcttgaacgcaca 60
    |||||||
DB 229 AATGCGATAGTAATGTGAATTGCAGAATTCAGTGAATCATCAATCTTGAACGCACA 288

QY 61 ttgcgccgcgaatlatctgcgcgcgcgttcgcgcgtcattcgaaccccaagcc 120
    |||||||
DB 289 TTGCGCCGCCGACGATTCGCGGCGCATGCTGTCAGCGCATATTCAACCCCTCAAGCC 348

QY 121 ccggggttggtgttgaggatcgcgaagcccttcgcgcgaagccgcgcgaatcagtg 180
    |||||||
DB 349 CCGGCGTTTGCTGTGGGATCGCGCGCTTCGCGCAAGCCGCCCGCAATCTAGTG 408

QY 181 ggcgttcgcgtcagcttcagtcgtaagtaaaacctgcgaactgtaagcgcg 240
    |||||||
DB 409 GCGGTCTGCTGCGAGCTTCATTCGAGTAGTAACCCCTCCAACTGTGACGCGCGC 468

QY 241 ggcgaagcgttlaaaccccaactctgaatgtgaacctgcgaactcgaatgaataccgc 300
    |||||||
DB 469 GGCCAAGCCCTTAAACCCCACTTGATGTGAACCTCGATCAGTAGTAATACCGG 528

QY 301 ctgaacttaa 310
    |||||||
DB 529 CTGAACCTTAA 538

RESULT 4
PPORRNA 558 bp DNA linear PLN 14-JUN-2001
LOCUS Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S
DEFINITION rRNA gene (partial), internal transcribed spacer 1 (ITS1) and
            internal transcribed spacer 2 (ITS2).
ACCESSION X94171.1 GI:1122873
VERSION 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;
            internal transcribed spacer 2; ITS1; ITS2.
SOURCE Fusarium proliferatum.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE 1 (bases 1 to 558)
AUTHORS Waalwijk, C., de Koning, J. R. A., Baayen, R. P., and Gams, W.
TITLE Discreet groupings of Fusarium spp. from sections Elegans,
JOURNAL liseola and diamantina a based on ribosomal ITS1 and ITS2 sequences
REFERENCE Mycologia 88, 361-368 (1996)
AUTHORS 2 (bases 1 to 358)
TITLE Waalwijk, C.
JOURNAL Direct Submission
AUTHORS Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Plant
COMMENT Protection, PO box 9060, 6700 GM Wageningen, NETHERLANDS
            On Jun 15, 2001 this sequence version replaced g1:1103572.

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FEATURES             Overlaps with X/8260.
source               Location/Qualifiers
                    1..558
                    /organism="Fusarium proliferatum"
                    /strain="CBS 217.76"
                    /specific_host="Cattleya"
                    /db_xref="taxon:42674"
                    <1..30
                    /gene="18S rRNA"
                    /product="18S ribosomal RNA"
gene 1..30
                    /gene="18S rRNA"
misc_feature 31..177
                    /note="Internal transcribed spacer 1, ITS1"
rRNA 178..335
                    /gene="5.8 rRNA"
                    /product="5.8 ribosomal RNA"
gene 178..335
                    /gene="5.8 rRNA"
misc_feature 336..500
                    /note="Internal transcribed spacer 2, ITS2"
rRNA 501..558
                    /gene="28S rRNA"
                    /product="28S ribosomal RNA"
gene 501..558
                    /gene="28S rRNA"
BASE COUNT 144 a 152 c 137 g 125 t
ORIGIN
Query Match 99.0%; Score 306.8; DB 8; Length 558;
Best Local Similarity 99.4%; Pred. No. 4.9e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaatgcataagtaatgtaattgcaaatctcagtaatcatcgaatcttgaacgcaca 60
    |||||||
DB 229 AATGCGATAGTAATGTGAATTGCAGAATTCAGTGAATCATCAATCTTGAACGCACA 288

QY 61 ttgcgccgcgaatlatctgcgcgcgcgttcgcgcgtcattcgaaccccaagcc 120
    |||||||
DB 289 TTGCGCCGCCGACGATTCGCGGCGCATGCTGTCAGCGCATATTCAACCCCTCAAGCC 348

QY 121 ccggggttggtgttgaggatcgcgaagcccttcgcgcgaagccgcgcgaatcagtg 180
    |||||||
DB 349 CCGGCGTTTGCTGTGGGATCGCGCGCTTCGCGCAAGCCGCCCGCAATCTAGTG 408

QY 181 ggcgttcgcgtcagcttcagtcgtaagtaaaacctgcgaactgtaagcgcg 240
    |||||||
DB 409 GCGGTCTGCTGCGAGCTTCATTCGAGTAGTAACCCCTCCAACTGTGACGCGCGC 468

QY 241 ggcgaagcgttlaaaccccaactctgaatgtgaacctgcgaactcgaatgaataccgc 300
    |||||||
DB 469 GGCCAAGCCCTTAAACCCCACTTGATGTGAACCTCGATCAGTAGTAATACCGG 528

QY 301 ctgaacttaa 310
    |||||||
DB 529 CTGAACCTTAA 538

RESULT 5
AF452163
LOCUS AF452163 569 bp DNA linear PLN 27-DEC-2001
DEFINITION Pythium ultimum var. sporangiferum isolate 308276r 18S ribosomal
            RNA gene, partial sequence.
ACCESSION AF452163
VERSION AF452163.1 GI:17980882
KEYWORDS Pythium ultimum var. sporangiferum.
SOURCE Pythium ultimum var. sporangiferum.
ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Pythium.
REFERENCE 1 (bases 1 to 569)
AUTHORS Moorman, G. W., Geiser, D. M., Kang, S., and Kim, S.

```

TITLE Pythium species and a population identification using DNA markers
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 569)
 AUTHORS Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
 TITLE Direct Submission
 JOURNAL Submitted (26-NOV-2001) Plant Pathology, Pennsylvania State University, 210 Buckhout Laboratory, University Park, PA 16802, USA

FEATURES
 source
 1..569
 /organism="Pythium ultimum var. sporangiferum"
 /variety="sporangiferum"
 /isolate="308276R"
 /db_xref="taxon:115421"
 <1..569
 /product="18S ribosomal RNA"

BASE COUNT 149 a 155 c 137 g 128 t
 ORIGIN

Query Match 99.0%: Score 306.8; DB 8; Length 569;
 Best Local Similarity 99.4%: Pred. No. 4.9e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aaatgcgataagtaatggaattgcaaaatcagtaataatcgaatccttgaacgcaca 60
 DB 246 AAATCGGATGAATGTAATGCAATTCAGATTCAGATTCGAATCTTTGAACGCACA 305
 OY 61 ttgcgccgcagatattctgcgagcgatgccttgcagagcattcaaccctcaagcc 120
 DB 306 TTGCGCCGCCAGATATTCGTGGCGGCATGCCTGTTCAGAGCTCATTTCAACCCCTCAAGCC 365
 OY 121 cccgggttggtgttggggatcggcaagcccttgcgcaagcggcccgaaatctagt 180
 DB 366 CCCGGTTGGTGTGGGGATCGCGAGCCCTTCGGCAGACCCGCCCGAAATCTAGTG 425
 OY 181 ggcgtctgcgcagcttccatctgtagtaataaaccccgcaactgtagcggcgcc 240
 DB 426 GCGGCTCGCTGCAGACTTCATTCGTAAGTAAACCCCGCACTGTAACCGCGCGC 485
 OY 241 ggcgaagccgttaaaccccaactctcgaatgtgacctcgatcaagtaggaataccg 300
 DB 486 GGCCAGCCGTTAAACCCCAACTTCGATGTGACCTCGATCAGTAGAATACCG 545
 OY 301 ctgaactaa 310
 DB 546 CTGAACCTTAA 555

RESULT 6
 AF291061 596 bp DNA linear PLN 18-SEP-2001
 LOCUS Fusarium proliferatum NRRL 31071 18S ribosomal RNA, partial
 DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and
 internal transcribed spacer 2, complete sequence; 28S ribosomal
 RNA, partial sequence.
 ACCESSION AF291061
 VERSION AF291061.1 GI:15637128
 KEYWORDS
 SOURCE Fusarium proliferatum.
 ORGANISM Fusarium proliferatum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
 REFERENCE 1 (bases 1 to 596)
 AUTHORS Kwon,S.-I., van Dohlon,C.D. and Anderson,A.J.
 TITLE Gene sequence analysis of an opportunistic wheat pathogen, an
 isolate of Fusarium proliferatum
 JOURNAL Can. J. Bot. 79 (9), 1115-1121 (2001)
 REFERENCE 2 (bases 1 to 596)
 AUTHORS Kwon,S.-I. and Anderson,A.J.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2000) Biology, Utah State University, Logan, UT
 84322-5305, USA
 FEATURES Location/Qualifiers

source 1..596
 /organism="Fusarium proliferatum"
 /strain="NRRL 31071"
 /specific_host="Triticum aestivum cv. Super Dwarf"
 /db_xref="taxon:42674"
 <1..596
 /note="contains 18S ribosomal RNA, internal transcribed
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
 2, 28S ribosomal RNA"

BASE COUNT 158 a 157 c 146 g 135 t
 ORIGIN

Query Match 99.0%: Score 306.8; DB 8; Length 596;
 Best Local Similarity 99.4%: Pred. No. 4.9e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aaatgcgataagtaatggaattgcaaaatcagtaataatcgaatccttgaacgcaca 60
 DB 267 AAATCGGATGAATGTAATGCAATTCAGATTCAGATTCGAATCTTTGAACGCACA 326
 OY 61 ttgcgccgcagatattctgcgagcgatgccttgcagagcattcaaccctcaagcc 120
 DB 327 TTGCGCCGCCAGATATTCGTGGCGGCATGCCTGTTCAGAGCTCATTTCAACCCCTCAAGCC 386
 OY 121 cccgggttggtgttggggatcggcaagcccttgcgcaagcggcccgaaatctagt 180
 DB 387 CCCGGTTGGTGTGGGGATCGCGAGCCCTTCGGCAGACCCGCCCGAAATCTAGTG 446
 OY 181 ggcgtctgcgcagcttccatctgtagtaataaaccccgcaactgtagcggcgcc 240
 DB 447 GCGGCTCGCTGCAGACTTCATTCGTAAGTAAACCCCTCGCAACTGTGACGCGCGC 506
 OY 241 ggcgaagccgttaaaccccaactctcgaatgtgacctcgatcaagtaggaataccg 300
 DB 507 GGCCAGCCGTTAAACCCCAACTTCGATGTGACCTCGATCAGTAGAATACCG 566
 OY 301 ctgaactaa 310
 DB 567 CTGAACCTTAA 576

RESULT 7
 AR168094 2293 bp DNA linear PAT 17-DEC-2001
 LOCUS AR168094
 DEFINITION Sequence 1 from patent US 6287800.
 ACCESSION AR168094
 VERSION AR168094.1 GI:17903914
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2293)
 AUTHORS Gallazzo,J.L. and Lee,M.D.
 TITLE Production of high titers of gibberellins, GA4 and GA7, by
 Gibberella fujikuroi strain LTB-1027
 JOURNAL Patent: US 6287800-A 1 11-SEP-2001;
 FEATURES Location/Qualifiers
 source 1..2293
 /organism="unknown"

BASE COUNT 596 a 527 c 592 g 578 t
 ORIGIN

Query Match 99.0%: Score 306.8; DB 6; Length 2293;
 Best Local Similarity 99.4%: Pred. No. 5.8e-84;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aaatgcgataagtaatggaattgcaaaatcagtaataatcgaatccttgaacgcaca 60
 DB 1972 AAATCGGATGAATGTAATGCAATTCAGATTCAGATTCGAATCTTTGAACGCACA 2031
 OY 61 ttgcgccgcagatattctgcgagcgatgccttgcagagcattcaaccctcaagcc 120

Db	2032	TTGGCCCGCCAGTATTCGTGGGGGCATGGCTGTTTCGAGCGTCATTTCAACCTTCAAGCC	2091
QY	121	CCGGAGTTGTGTGTGGGATCGGCAAGCCCTGGCGAAGCGGCCCGAATTAgt	180
Db	2092	CCCGGATTGGGTGGGGGATGGCGAGCCCTTGGCGCAAGCGGGCCCGAATTAgtg	2151
QY	181	GCgATCgCtgcAtgcAtCtCtCaCtTgcTgaTgaTaaacCctgcCaCtTgtAcgcGgcgc	240
Db	2152	CGCGTCTCGCTCCACCTTCACATTCGTAGTAAACCTTCGCAACTGTCGCGCGC	2211
QY	241	ggccaaacCGTtaaaccCcccaactCtgaatgtTgaCctCggaTaaagTaaataaccg	300
Db	2212	GGCCAAGCGTTAAACCCCAACTTCTGAATTTTACCTCGATGAGGTAGAAATACCG	2271
QY	301	Ctgaacttaa	310
Db	2272	CTGAACTTAA	2281

RESULT	8	
AF158303		
LOCUS	531 bp	DNA
DEFINITION	Fusarium sp. NRRL26794 18S ribosomal RNA gene, partial sequence; Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.	
ACCESSION	AF158303	
VERSION	AF158303.1	GI:7106206
KEYWORDS		
SOURCE	Fusarium sp. NRRL26794.	
ORGANISM	Fusarium sp. NRRL26794.	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.	
AUTHORS	1 (bases 1 to 531)	
TITLE	O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.	
	A multigene phylogeny of the gibberella fujikuroi species complex: detection of additional phylogenetically distinct species	
	Mycoscience 41, 61-78 (2000)	
JOURNAL	2 (bases 1 to 531)	
REFERENCE	O'Donnell,K.	
AUTHORS	Direct Submission	
TITLE	Submitted (10-JUN-1999) Microbial Properties, NCAR-USDA-ARS, 1815	
JOURNAL	N. University St., Peoria, IL 61604, USA	
FEATURES	Location/Qualifiers	
Source	1..531	
	/organism="Fusarium sp. NRRL26794"	
	/strain="NRRL26794"	
	/db_xref="taxon:100621"	
	<1..23	
rRNA	24..169	
	/product="18S ribosomal RNA"	
misc_RNA	170..328	
	/product="Internal transcribed spacer 1"	
rRNA	329..493	
	/product="5.8S ribosomal RNA"	
misc_RNA	494..>531	
	/product="Internal transcribed spacer 2"	
rRNA	494..>531	
	/product="28S ribosomal RNA"	
BASE COUNT	137 a	146 c 128 g 120 t
ORIGIN		

Query Match	98.5%	Score 305.2;	DB: 8;	Length 531;	
Best Local Similarity	99.0%;	Pred. No. 1.5e-83;			
Matches 307;	Conservative 0;	Matches 3;	Indels 0;	Gaps 0;	
Qy	1	aatgcgaataa	tgatgcaaat	taagaaatcaagatcgaatcttgaacgaca	60
Db	222	AAATCGAATAGTATGTGAATGCCAAGATTGACGATCATCGAATCTTGAACGACA			281
Oy	61	ttgcgcgcgaagatattcgcgcggcagatcctgttgcagcgatattcaaccctcaagc			120

Dd	282	TTGGCCCGCAGTATTCCTG6GGGACGATGCTGTTCGAGGTCATATTCAACCCTCAAGCC	341
Qy	121	cccgagtttgtagtgcgggacgcgaagccctgcgcgaagccggccccgaatcagtg	180
Dd	342	CTCGGGTTTTGGTGTTGGGGGATCGGGGACCCCTTGGCGCAACCCGGCCCCGAATCTACTG	401
Qy	181	gcgcgtcgcgcgcgaacttcacattgcgtagttagtaaacccctcgcaactcgtgtaacgcgcgc	240
Dd	402	GCGGCTCTGGCTGCACCTTCCATTGGGTAAGTAAACCCCTCGCAACTGTAACGGGGCC	461
Qy	241	ggccaagccgctaaaccccccaactcctlctaagctltgacctcgatacgaagtagaataaccg	300
Dd	462	GGCCAAGCCGTTAAACCCCAACTCTGAATGTTGACCTCGGATCAGGTAGGAATACCG	521
Qy	301	ctgaacttaa	310
Dd	522	CTGAACCTTAA	531

RESULT 9
 AF158304
 LOCUS
 DEFINITION
 AF158304
 540 bp DNA linear PLN 21-MAR-2000
 Fusarium sp. NRRL28852 18S ribosomal RNA gene, partial sequence;
 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 AF158304
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Fusarium sp. NRRL28852.
 Fusarium sp. NRRL28852.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 540)
 O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigcelink, E.
 A multigene phylogeny of the Gibberella fujikuroi species complex:
 detection of additional phylogenetically distinct species
 Mycoscience 41, 61-78 (2000)
 2 (bases 1 to 540)
 O'Donnell, K.
 Direct Submission
 Submitted (10-JUN-1999) Microbial Properties, NCAR-USDA-ARS, 1815
 N. University St., Peoria, IL 61604, USA
 Location/Qualifiers
 1..540
 source

	Query Match	Best Local Similarity	98.5%	Score 305.2	DB 8	Length 540
Matches	307	Conservative	0	Mismatches 3	Indels 0	Gaps 0
Oy	1	aaatgcgaataagtaagtcgaataatcgaataatcgaatcgaatcgttgaaagcaca	60			
Db	231	AAATCGATAGTAATGGAATTGCGACATTCAGATGATCATCGATCTTTGAACGCCACA	290			
Oy	61	ttgcgccccgcaagtaattctggcgcgagcctgctgttcgagcgtcattcaaccctcaagcc	120			
Db	291	TTGCGCCCGCCAGTTTGTTCGCGGGCAGCTGTTTCGAGCTCATTTTCAACCTTCAAGCC	350			

OY 121 ccggggttggtgttggtggtatcggaagcccttgcggaagccgcccgaatctagt 180
 |||
 Db 351 CCCGGGTTTGTTGGGATCGCGAGCCCTCGCGCAAGCCGCGCCCAATATTAGTG 410
 OY 181 ggggttcgctgcagcttcacatgtagtaagtaaaccttcgcaactgtagcgagc 240
 |||
 Db 411 GCGGTCTGCTGAGCTTCACTTGCAGTAGTAATAACCTCGCACTGATACGCGCGC 470
 OY 241 gggcaagccgttaaaccccccaacttcgtaattgtagcttcgtagtgtaataccg 300
 |||
 Db 471 GGCACAGCCGTTAAACCCCAACTTGTGAATGTTGACCTGGATCAGTAGAATACCCG 530
 OY 301 ctgaactaa 310
 |||
 Db 531 CTGAACCTTAA 540

RESULT 10
 AF158302 540 bp DNA linear PLN 21-MAR-2000
 LOCUS Fusarium sp. NRRL26427 18S ribosomal RNA gene, partial sequence;
 DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 ACCESSION AF158302.1 GI:7106205
 VERSION AF158302
 KEYWORDS
 SOURCE Fusarium sp. NRRL26427.
 ORGANISM Fusarium sp. NRRL26427
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 540)
 O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigelnik, E.
 A multigenic phylogeny of the Gibberella fujikuroi species complex:
 detection of additional phylogenetically distinct species
 Mycoscience 41, 61-78 (2000)
 2 (bases 1 to 540)
 O'Donnell, K.
 Direct Submission
 Submitted (10-JUN-1999) Microbial Properties, NCAUR-USDA-ARS, 1815
 University St., Peoria, IL 61604, USA
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..540
 /organism="Fusarium sp. NRRL26427"
 /strain="NRRL26427"
 /db_xref="taxon:100620"
 <1..32
 rRNA /product="18S ribosomal RNA"
 33..178
 misc_RNA /product="internal transcribed spacer 1"
 179..337
 rRNA /product="5.8S ribosomal RNA"
 338..502
 misc_RNA /product="internal transcribed spacer 2"
 503..>540
 rRNA /product="28S ribosomal RNA"
 BASE COUNT 137 a 150 c 130 g 123 t
 ORIGIN

Query Match 97.9% Score 303.6; DB 8; Length 540;
 Best Local Similarity 98.7% Pred. No. 4.7e-83;
 Matches 306; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 aatgcatgaagtaagtgaatgcaaatcagtgatcatcgaatcttgaagcaca 60
 |||
 Db 231 AATGCGATTAAGTAATGTAATGCAAGATTGAGTAATCATGAAATCTTGAACGACA 290
 OY 61 ttggcgccgacgatactctggcgagcagtcctgttcgagcgtaattcaaccctaaagc 120
 |||
 Db 291 TTGGCGCCCGCAGTAATTTGGCGGAGTGCCTGTTCGAGCGTCAATTCACCTCAAGCC 350

OY 121 ccggggttggtgttggtggtatcggaagcccttgcggaagccgcccgaatctagt 180
 |||
 Db 351 CCCGGGTTTGTTGGGATCGCGAGCCCTCGCGCAAGCCGCGCCCAATATTAGTG 410
 OY 181 ggggttcgctgcagcttcacatgtagtaagtaaaccttcgcaactgtagcgagc 240
 |||
 Db 411 GCGGTCTGCTGAGCTTCACTTGCAGTAGTAATAACCTCGCACTGATACGCGCGC 470
 OY 241 gggcaagccgttaaaccccccaacttcgtaattgtagcttcgtagtgtaataccg 300
 |||
 Db 471 GGCACAGCCGTTAAACCCCAACTTGTGAATGTTGACCTGGATCAGTAGAATACCCG 530
 OY 301 ctgaactaa 310
 |||
 Db 531 CTGAACCTTAA 540

RESULT 11
 FJ34557 534 bp DNA linear PLN 15-JUL-1998
 LOCUS Fusarium fujikuroi internal transcribed spacer RNA.
 DEFINITION U34557
 ACCESSION U34557.1 GI:1808928
 VERSION U34557.1
 KEYWORDS
 SOURCE Gibberella fujikuroi.
 ORGANISM Gibberella fujikuroi.
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE 1 (bases 1 to 534)
 O'Donnell, K. and Cigelnik, E.
 Two divergent intragenomic rDNA ITS2 types within a monophyletic
 lineage of the fungus Fusarium are nonorthologous
 Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
 2 (bases 1 to 534)
 O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.
 Molecular systematics and phylogeography of the Gibberella
 fujikuroi species complex
 Mycologia 90 (3), 465-493 (1998)
 3 (bases 1 to 534)
 O'Donnell, K. and Cigelnik, E.
 Direct Submission
 Submitted (21-AUG-1995) Kerry O'Donnell, NCAUR, USDA, 1815 N.
 University St., Peoria, IL 61604, USA
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..534
 /organism="Gibberella fujikuroi"
 /strain="NRRL 13566"
 /db_xref="taxon:5127"
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 misc_RNA /product="internal transcribed spacer"
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 ORIGIN

Query Match 97.7% Score 302.8; DB 8; Length 534;
 Best Local Similarity 99.3% Pred. No. 8.4e-83;
 Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 aatgcatgaagtaagtgaatgcaaatcagtgatcatcgaatcttgaagcaca 60
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 Db 229 AATGCGATTAAGTAATGTAATGCAAGATTGAGTAATCATGAAATCTTGAACGACA 288
 OY 61 ttggcgccgacgatactctggcgagcagtcctgttcgagcgtaattcaaccctaaagc 120
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 Db 289 TTGGCGCCCGCAGTAATTTGGCGGAGTGCCTGTTCGAGCGTCAATTCACCTCAAGCC 348
 OY 121 ccggggttggtgttggtggtatcggaagcccttgcggaagccgcccgaatctagt 180
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 Db 349 CCCGGGTTTGTTGGGATCGCGAGCCCTTTCGCGCAAGCCGCGCAATATTAGTG 408
 OY 181 ggggttcgctgcagcttcacatgtagtaagtaaaccttcgcaactgtagcgagc 240
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RESULT 8
US-08-737-129A-5/C
: Sequence 5, Application US/08737129A
: Patent No. 5885816
: GENERAL INFORMATION:
: APPLICANT: Ikao FUJII et al.
: TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
: TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/737,129A
: FILING DATE: No. 5885816member 15, 1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warren M. Cheek, Jr.
: REGISTRATION NUMBER: 33,367
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-8850
: TELEFAX:
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 666 bases
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-737-129A-5

Query Match 77.8%; Score 14; DB 2; Length 666;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtcgcgt 18
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Db 596 GTGACGCTCGCT 583

RESULT 9
PCT-US94-14106-58/C
: Sequence 58, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14106
: FILING DATE:
: CLASSIFICATION:
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: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 717 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 67..717
: PCT-US94-14106-58

Query Match 77.8%; Score 14; DB 5; Length 717;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtcgcgt 18
|||||
Db 653 GTGACGCTCGCT 640

RESULT 10
PCT-US94-14106-50/C
: Sequence 50, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14106
: FILING DATE:
: CLASSIFICATION:
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 735 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 67..735
: PCT-US94-14106-50

Query Match 77.8%; Score 14; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtcgcgt 18
|||||
Db 671 GTGACGCTCGCT 658

RESULT 11
PCT-US94-14106-54/C
: Sequence 54, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..735
PCT-US94-14106-54

Query Match 77.8%; Score 14; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||
DB 671 GTGACGCTCTCGCT 658

RESULT 12
US-08-860-882A-25/c
Sequence 25, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HOW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-25

Query Match 77.8%; Score 14; DB 2; Length 777;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||
DB 677 GTGACGCTCTCGCT 664

RESULT 13
US-08-133-011-99/c
Sequence 99, Application US/08133011
Patent No. 5658727
GENERAL INFORMATION:
APPLICANT: Kang, Andray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-133-011-99

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
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Db 695 GTGACGCTCGCT 682

RESULT 14

US-08-322-730A-99/C
Sequence 99, Application US/08322730A
Patent No. 5759817

GENERAL INFORMATION:

APPLICANT: Bardas, Carlos

TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING

TITLE OF INVENTION: PHAGEMIDS

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/322,730A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/826,623

FILING DATE: 27-JAN-1992

APPLICATION NUMBER: US 07/683,602

FILING DATE: 10-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bingham, Douglas A

REGISTRATION NUMBER: 32,457

REFERENCE/DOCKET NUMBER: SCRO707P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-784-2937

TELEFAX: 619-784-9399

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-322-730A-99

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 695 GTGACGCTCGCT 682

RESULT 15

US-08-387-874-71/C
Sequence 71, Application US/08387874
Patent No. 5770356

GENERAL INFORMATION:

APPLICANT: Light, Paul L., II

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: PHAGEMIDS COEXPRESSION A SURFACE

TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874

FILING DATE: 22-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08364

FILING DATE: 03-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,369

FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Filling, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 303.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-6312

TELEFAX: 619-554-2937

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-387-874-71

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gtgacgctcgcct 18
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Db 695 GTGACGCTCGCT 682

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Job time: 5702 sec

Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-046-955-49
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16.4	91.1	310	US-09-423-233-7	Sequence 7, Appl1
3	16.4	91.1	534	US-09-961-755A-7	Sequence 7, Appl1
4	16.4	91.1	637	US-09-580-797-12	Sequence 12, Appl
5	15.4	85.6	218	US-09-270-849B-60978	Sequence 60978, A
6	15.4	85.6	279	US-09-594-745-22526	Sequence 22526, A
7	15.4	85.6	279	US-09-565-306-46194	Sequence 46194, A
8	15.4	85.6	279	US-09-654-617-323951	Sequence 323951, A
9	15.4	85.6	279	US-09-684-016-323951	Sequence 323951, A
10	15.4	85.6	443	US-09-270-849B-105057	Sequence 105057, A
11	15.4	85.6	592	US-09-505-532-22896	Sequence 22896, A
12	15.4	85.6	592	US-09-819-091A-22896	Sequence 22896, A
13	15.4	85.6	744	US-09-708-427-6695	Sequence 6695, Ap
14	15.4	85.6	879	US-09-270-849B-124742	Sequence 124742, A
15	15.4	85.6	1123	US-09-620-392-4174	Sequence 4174, Ap
16	15.4	85.6	7555	US-09-620-392-10798	Sequence 10798, A
17	15.4	85.6	9852	US-09-620-392-10798	Sequence 10798, A
18	15.4	85.6	14744	US-09-702-134-4847	Sequence 4847, Ap
19	15.4	85.6	14744	US-09-815-264-82429	Sequence 82429, A
20	15.4	85.6	78341	US-09-534-859-4	Sequence 4, Appl1
21	15.4	85.6	78341	US-09-803-736-4	Sequence 4, Appl1
22	15	83.3	143	US-09-342-217-2185	Sequence 2185, Ap
23	15	83.3	143	US-09-342-217-2185	Sequence 2185, Ap
24	15	83.3	241	US-08-728-362-1069	Sequence 1069, Ap
25	15	83.3	241	US-08-992-332-1069	Sequence 1069, Ap
26	15	83.3	241	US-60-005-019-1069	Sequence 1069, Ap
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28	15	83.3	245	US-08-330-011-2992	Sequence 2992, Ap
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31	15	83.3	249	US-09-540-229-116567	Sequence 116567, A

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C 33 15 83.3 264 20 US-09-539-806-41390 Sequence 41390, A
C 34 15 83.3 277 21 US-09-540-229-114380 Sequence 114380,
C 35 15 83.3 277 21 US-09-540-766-58240 Sequence 58240, A
C 36 15 83.3 280 17 US-09-321-214-18008 Sequence 18008, A
C 37 15 83.3 280 19 US-09-516-335-18008 Sequence 18008, A
C 38 15 83.3 280 29 US-09-733-811-18008 Sequence 18008, A
C 39 15 83.3 280 29 US-09-733-811A-18008 Sequence 18008, A
C 40 15 83.3 280 36 US-09-975-640-18008 Sequence 18008, A
C 41 15 83.3 281 21 US-09-975-640A-18008 Sequence 18008, A
C 42 15 83.3 281 21 US-09-540-764-49406 Sequence 49406, A
C 43 15 83.3 293 5 US-08-196-363-4820 Sequence 4820, Ap
C 44 15 83.3 293 5 US-08-196-363A-4820 Sequence 4820, Ap
C 45 15 83.3 293 5 US-08-196-363-4820 Sequence 4820, Ap
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ALIGNMENTS

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RESULT 1
US-09-423-233-49
; Sequence 49, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-49
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Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctagtgcggtctcgct 18
   |||||
Db 1 tctagtgcggtctcgct 18

RESULT 2
US-09-423-233-7
; Sequence 7, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7
```

```
Query Match 91.1%; Score 16.4; DB 18; Length 310;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtgcggtctcgct 18
   |||||
Db 174 tctagtgcggtctcgct 191
```

```
RESULT 3
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7
```

```
Query Match 91.1%; Score 16.4; DB 36; Length 534;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtgcggtctcgct 18
   |||||
Db 402 tctagtgcggtctcgct 419
```

```
RESULT 4
US-09-580-797-12
; Sequence 12, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Fusarium moniliformes
US-09-580-797-12
```

```
Query Match 91.1%; Score 16.4; DB 22; Length 637;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtgcggtctcgct 18
   |||||
Db 514 tctagtgcggtctcgct 531
```

```
RESULT 5
US-09-270-849B-60978
; Sequence 60978, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
```



```
; SEQ ID NO 60978
; LENGTH: 218
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-60978
```

```
Query Match      85.6%; Score 15.4; DB 16; Length 218;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 ctatgacggtctcgct 18
|||||
DB 41 ctatgacggtctcgct 57

```
RESULT 6
US-09-394-745-22526
; Sequence 22526, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalugui, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 22526
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3066-031-Q1-E1-F12
US-09-394-745-22526
```

```
Query Match      85.6%; Score 15.4; DB 17; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 ctatgacggtctcgct 18
|||||
DB 82 cgagtgacggtctcgct 98

```
RESULT 7
US-09-565-306-46194
; Sequence 46194, Application US/09565306
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalugui, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15459)C
; CURRENT APPLICATION NUMBER: US/09/565,306
; CURRENT FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 46194
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3066-031-Q1-E1-F12
US-09-565-306-46194
```

```
Query Match      85.6%; Score 15.4; DB 22; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 ctatgacggtctcgct 18

DB 82 cgagtgacggtctcgct 98

```
RESULT 8
US-09-654-617-323951
; Sequence 323951, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 323951
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
US-09-654-617-323951
```

```
Query Match      85.6%; Score 15.4; DB 25; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 ctatgacggtctcgct 18
|||||
DB 82 cgagtgacggtctcgct 98

```
RESULT 9
US-09-684-016-323951
; Sequence 323951, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 323951
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-323951
```

```
Query Match      85.6%; Score 15.4; DB 27; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 ctatgacggtctcgct 18
|||||
DB 82 cgagtgacggtctcgct 98

```
RESULT 10
US-09-270-849B-105057
; Sequence 105057, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105057
; LENGTH: 443
```

```
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-105057
```

```
Query Match      85.6% Score 15.4; DB 16; Length 443;
Best Local Similarity 94.1% Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1  tctagtgcggtctgcg 17
          ||||| ||||| |||||
DB      253 tctagtgcggtctgcg 269
```

```
RESULT 11
US-09-505-532-22896
Sequence 22896, Application US/09505532
```

```
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478)B
CURRENT APPLICATION NUMBER: US/09/505,532
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 22896
LENGTH: 592
TYPE: DNA
ORGANISM: Arabidopsis thaliana columbia
OTHER INFORMATION: unsure at all n locations
US-09-505-532-22896
```

```
Query Match      85.6% Score 15.4; DB 19; Length 592;
Best Local Similarity 94.1% Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2  ctatgcggtctgcgt 18
          ||||| ||||| |||||
DB      201 ctatgcggtctgcgt 217
```

```
RESULT 12
US-09-819-091A-22896
Sequence 22896, Application US/09819091A
```

```
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478)B
CURRENT APPLICATION NUMBER: US/09/819,091A
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: US 60/108,420
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 09/443,025
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 22896
LENGTH: 592
TYPE: DNA
ORGANISM: Arabidopsis thaliana columbia
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(592)
OTHER INFORMATION: unsure at all n locations
US-09-819-091A-22896
```

```
Query Match      85.6% Score 15.4; DB 31; Length 592;
Best Local Similarity 94.1% Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2  ctatgcggtctgcgt 18
          ||||| ||||| |||||
DB      201 ctatgcggtctgcgt 217
```

```
RESULT 13
US-09-708-427-6695
Sequence 6695, Application US/09708427
```

```
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6695
LENGTH: 744
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..744
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
LOCATION: 1..744
NAME/KEY: misc.feature
OTHER INFORMATION: Ceres Seq. ID 1816224
US-09-708-427-6695
```

```
Query Match      85.6% Score 15.4; DB 28; Length 744;
Best Local Similarity 94.1% Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2  ctatgcggtctgcgt 18
          ||||| ||||| |||||
DB      218 ctatgcggtctgcgt 234
```

```
RESULT 14
```

```
US-09-270-849B-124742/C
Sequence 124742, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 124742
LENGTH: 879
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-124742
```

```
Query Match      85.6% Score 15.4; DB 16; Length 879;
Best Local Similarity 94.1% Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2  ctatgcggtctgcgt 18
          ||||| ||||| |||||
DB      482 ctatgcggtctgcgt 466
```

RESULT 15
US-09-270-849B-139165/C
; Sequence 139165, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139165
; LENGTH: 1123
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-139165

Query Match 85.6%; Score 15.4; DB 16; Length 1123;
Best Local Similarity 94.1%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctagtacggtctcgct 18
1 |||||
DB 279 CGAGTGCAGCTCTCGCT 263

Search completed: August 22, 2002, 00:39:32
Job time: 13057 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:50 ; Search time 663.62 Seconds
(without alignments)
72.981 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 1 tctagtacggtctcgct 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1721111 seqs, 1345317543 residues

Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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8: /cgn2_6/pdata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	7	US-10-046-955-49
2	16.4	91.1	310	7	US-10-046-955-7
3	15	83.3	386	5	US-09-918-995-33508
4	15	83.3	449	5	US-09-918-995-34287
5	15	83.3	473	5	US-09-918-995-1024
6	15	83.3	1624	5	US-09-919-002-3535
7	14.8	82.2	403	5	US-09-785-276A-2782
8	14.8	82.2	599	7	US-10-027-632-215234
9	14.8	82.2	599	7	US-10-027-632-215235
10	14.8	82.2	1192	6	US-10-098-754-3118
11	14.8	82.2	1549	5	US-09-634-754C-156
12	14.8	82.2	1549	5	US-09-634-754D-156
13	14.8	82.2	25593	1	PCT-US02-14011-1
14	14.8	82.2	277	5	US-09-539-331D-39667
15	14.8	82.2	295	5	US-09-540-210B-17019
16	14.8	77.8	736	7	US-10-006-773-12
17	14.8	77.8	1666	6	US-10-098-754-10959
18	14.8	77.8	1800	7	US-10-170-155-6
19	14.8	77.8	2140	1	PCT-US02-22866-42
20	14.8	77.8	4191	7	US-10-176-380-18
21	14.8	77.8	5691	5	US-09-897-511A-11
22	14.8	77.8	5711	5	US-09-897-511A-8
23	14.8	77.8	6255	5	US-09-887-511A-13
24	13.8	76.7	25	5	US-09-396-196G-117408
25	13.8	76.7	220	7	US-10-137-316-56

26	13.8	76.7	309	5	US-09-540-210B-34640	Sequence 34640, A
27	13.8	76.7	319	7	US-10-137-316-10	Sequence 10, Appl
28	13.8	76.7	319	7	US-10-137-316-40	Sequence 40, Appl
29	13.8	76.7	371	5	US-09-785-276A-12650	Sequence 12650, A
30	13.8	76.7	373	5	US-09-785-276A-3481	Sequence 3481, Ap
31	13.8	76.7	383	5	US-09-785-276A-11609	Sequence 11609, A
32	13.8	76.7	384	5	US-09-785-276A-11951	Sequence 11951, A
33	13.8	76.7	403	5	US-09-785-276A-10948	Sequence 10948, A
34	13.8	76.7	410	5	US-09-785-276A-37090	Sequence 37090, A
35	13.8	76.7	410	5	US-09-785-276A-41707	Sequence 41707, A
36	13.8	76.7	413	5	US-09-785-276A-12666	Sequence 12666, A
37	13.8	76.7	413	5	US-09-785-276A-33807	Sequence 33807, A
38	13.8	76.7	415	5	US-09-785-276A-7121	Sequence 7121, Ap
39	13.8	76.7	418	5	US-09-785-276A-32781	Sequence 32781, A
40	13.8	76.7	419	5	US-09-785-276A-33123	Sequence 33123, A
41	13.8	76.7	419	5	US-09-785-276A-42049	Sequence 42049, A
42	13.8	76.7	420	5	US-09-785-276A-2440	Sequence 2440, Ap
43	13.8	76.7	432	7	US-10-137-316-27	Sequence 27, Appl
44	13.8	76.7	443	5	US-09-785-276A-32125	Sequence 32125, A
45	13.8	76.7	443	5	US-09-785-276A-40220	Sequence 40220, A

ALIGNMENTS

RESULT 1
US-10-046-955-49
Sequence 49, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Errol
APPLICANT: Aldorevich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-49

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
|||||
Db 1 tctagtacggtctcgct 18

RESULT 2
US-10-046-955-7
Sequence 7, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.

```
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Seo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7
```

```
Query Match          91.1%; Score 16.4; DB 7; Length 310;
Best Local Similarity 94.4%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 tctagtgcggtctgcgt 18
Db 174 tctagtgcggtctgcgt 191
```

```
RESULT 3
US-09-918-995-33508/c
; Sequence 33508, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: FROM VARIOUS CDNA LIBRARIES
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33508
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33508
```

```
Query Match          83.3%; Score 15; DB 5; Length 386;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 208 agtgacggtctgcgt 194
```

```
RESULT 4
US-09-918-995-34287/c
; Sequence 34287, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: FROM VARIOUS CDNA LIBRARIES
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 13203
```

```
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34287
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-34287
```

```
Query Match          83.3%; Score 15; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 253 agtgacggtctgcgt 239
```

```
RESULT 5
US-09-918-995-1024/c
; Sequence 1024, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: FROM VARIOUS CDNA LIBRARIES
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1024
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1024
```

```
Query Match          83.3%; Score 15; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 230 agtgacggtctgcgt 216
```

```
RESULT 6
US-09-919-002-3555
; Sequence 3555, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
```

```
SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3555
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-3555
```

```
Query Match      83.3%  Score 15:  DB 5:  Length 1624;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15:  Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4  agtgcgcgtcgcgt 18
          |||
Db      1387 agtgcgcgtcgcgt 1401
```

```
RESULT      7
US-09-785-276A-2782/c
; Sequence 2782, Application US/09785276A
```

```
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
```

```
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
```

```
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
```

```
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
```

```
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
```

```
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
```

```
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2782
```

```
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 211_216, 362, 364
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2782
```

```
Query Match      82.2%  Score 14.8;  DB 5:  Length 403;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1  tctagtgcgcgtcgcgt 18
          |||
Db      350  tctagtgcgcgtcgcgt 333
```

```
RESULT      8
US-10-027-632-215234
; Sequence 215234, Application US/10027632
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
```

```
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 215234
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215234
```

```
Query Match      82.2%  Score 14.8;  DB 7:  Length 599;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1  tctagtgcgcgtcgcgt 18
          |||
Db      206  tctagtgcgcgtcgcgt 223
```

```
RESULT      9
US-10-027-632-215235
; Sequence 215235, Application US/10027632
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```

```
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 215235
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215235
```

```
Query Match      82.2%  Score 14.8;  DB 7:  Length 599;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1  tctagtgcgcgtcgcgt 18
          |||
Db      206  tctagtgcgcgtcgcgt 223
```

```
RESULT 10
US-10-098-754-3118
; Sequence 3118, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundle, Stephen E.
; APPLICANT: Ramchandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: ATX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIORITY FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 2107
; SOFTWARE: FASTED for Windows Version 4.0
; SEQ ID NO 3118
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1192)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-3118

Query Match      82.2%  Score 14.8;  DB 6;  Length 1192;
Best Local Similarity 88.9%;  Pred. No. 1.3e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  tctagtgcgcgtcgcgt 18
        |||||  |||||  |||||  |||||
DB      748  tctagtgcgcgtcgcgt 765

RESULT 11
US-09-634-754C-156/C
; Sequence 156, Application US/09634754C
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/09/634,754C
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 156
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2822724CT1
; PUBLICATION INFORMATION:
US-09-634-754C-156

Query Match      82.2%  Score 14.8;  DB 5;  Length 1549;
Best Local Similarity 88.9%;  Pred. No. 1.3e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  tctagtgcgcgtcgcgt 18
        |||||  |||||  |||||  |||||
DB      343  tctagtgcgcgtcgcgt 326
```

```
RESULT 12
US-09-634-754D-156/C
; Sequence 156, Application US/09634754D
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/09/634,754D
; CURRENT FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 156
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2822724CT1
; PUBLICATION INFORMATION:
US-09-634-754D-156

Query Match      82.2%  Score 14.8;  DB 5;  Length 1549;
Best Local Similarity 88.9%;  Pred. No. 1.3e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  tctagtgcgcgtcgcgt 18
        |||||  |||||  |||||  |||||
DB      343  tctagtgcgcgtcgcgt 326

RESULT 13
PCT-US02-14011-1/C
; Sequence 1, Application PCT/US0214011
; GENERAL INFORMATION:
; APPLICANT: Genesance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshy, Beena
; APPLICANT: Sankar, Angela
; APPLICANT: Sankar, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRA GENE
; FILE REFERENCE: MMH-0838PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14011
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,475
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 25593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7648)..(7648)
; OTHER INFORMATION: PS1: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7685)..(7685)
; OTHER INFORMATION: PS2: polymorphic base adenine or cytosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12702)..(12801)
; OTHER INFORMATION: N's represent breaks between Genesance Reference Nos. 468376
; OTHER INFORMATION: 4683871
; FEATURE:
```

```
NAME/KEY: allele
LOCATION: (14001)..(14001)
OTHER INFORMATION: PS3: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15098)..(15197)
OTHER INFORMATION: N's represent breaks between Genalissance Reference Nos. 4683871 &
OTHER INFORMATION: 4683825
FEATURE:
NAME/KEY: allele
LOCATION: (15759)..(15759)
OTHER INFORMATION: PS4: polymorphic base guanine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (16071)..(16071)
OTHER INFORMATION: PS5: polymorphic base cytosine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (16077)..(16077)
OTHER INFORMATION: PS6: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (16124)..(16124)
OTHER INFORMATION: PS7: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16521)..(16620)
OTHER INFORMATION: N's represent breaks between Genalissance Reference Nos. 4683825 &
OTHER INFORMATION: 4683835
FEATURE:
NAME/KEY: allele
LOCATION: (17688)..(17688)
OTHER INFORMATION: PS8: polymorphic base thymine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (17989)..(17989)
OTHER INFORMATION: PS9: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18377)..(18377)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18417)..(18417)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18461)..(18461)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18469)..(18469)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: allele
LOCATION: (20395)..(20395)
OTHER INFORMATION: PS10: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (20488)..(20488)
OTHER INFORMATION: PS11: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (20542)..(20542)
OTHER INFORMATION: PS12: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (20779)..(20779)
OTHER INFORMATION: PS13: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21779)..(21878)
OTHER INFORMATION: N's represent breaks between Genalissance Reference Nos. 4683835
```

```
OTHER INFORMATION: and 4683853
FEATURE:
NAME/KEY: allele
LOCATION: (22016)..(22016)
OTHER INFORMATION: PS14: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (22040)..(22040)
OTHER INFORMATION: PS15: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22076)..(22076)
OTHER INFORMATION: PS16: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (22090)..(22090)
OTHER INFORMATION: PS17: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22117)..(22117)
OTHER INFORMATION: PS18: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22320)..(22320)
OTHER INFORMATION: PS19: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (24434)..(24434)
OTHER INFORMATION: PS20: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (24462)..(24462)
OTHER INFORMATION: PS21: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (24504)..(24504)
OTHER INFORMATION: PS22: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (24660)..(24660)
OTHER INFORMATION: PS23: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (24824)..(24824)
OTHER INFORMATION: PS24: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (24917)..(24917)
OTHER INFORMATION: PS25: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (25048)..(25048)
OTHER INFORMATION: PS26: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (25185)..(25185)
OTHER INFORMATION: PS27: polymorphic base cytosine or thymine
PCT-US02-14011-1
```

```
Query Match      82.2%  Score 14.8:  DB 1:  Length 25593;
Best Local Similarity  88.9%  Pred No. 1.4e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
```

QY 1 tctagtgcaggtctcgct 18
||||| | ||||| |
Db 6169 TCTAGTGCTGCTCGCT 6152

```
RESULT 14  
US-09-539-331D-39667/c  
; Sequence 39667, Application US/09539331D  
; GENERAL INFORMATION:
```



```

: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539,331D
: CURRENT FILING DATE: 2000-03-30
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 39667
: LENGTH: 277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No: hu00747836
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 26, 38, 55, 70, 111, 124, 126, 128, 134, 147, 150-151, 168, 171, 189,
: LOCATION: 191, 209, 235, 238, 241, 258, 275
: OTHER INFORMATION: a, t, c, g, or other
: US-09-539-331D-39667

Query Match          77.8%: Score 14; DB 5; Length 277;
Best Local Similarity 93.3%: Pred. No. 3.7e+02;
Matches 14: Conservative 1; Indels 0; Gaps 0;

QY 4 agtgcaggtctgcct 18
DB 37 ACTGACGGCTGCTGCT 23

RESULT 15
US-09-540-210B-17019/c
: Sequence 17019, Application US/09540210B
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
: FILE REFERENCE: PD-1037 CIP
: CURRENT APPLICATION NUMBER: US/09/540,210B
: CURRENT FILING DATE: 2002-04-03
: PRIOR APPLICATION NUMBER: 08/972,899
: PRIOR FILING DATE: November 18, 1997
: PRIOR APPLICATION NUMBER: 08/395,244
: PRIOR FILING DATE: February 27, 1995
: PRIOR APPLICATION NUMBER: 08/722,922
: PRIOR FILING DATE: September 27, 1996
: PRIOR APPLICATION NUMBER: 60/005,526
: PRIOR FILING DATE: September 29, 1995
: PRIOR APPLICATION NUMBER: 08/824,029
: PRIOR FILING DATE: March 25, 1997
: PRIOR APPLICATION NUMBER: 60/014,010
: PRIOR FILING DATE: March 25, 1996
: PRIOR APPLICATION NUMBER: 08/826,847
: PRIOR FILING DATE: April 10, 1997
: PRIOR APPLICATION NUMBER: 60/015,533
: PRIOR FILING DATE: April 10, 1996
: PRIOR APPLICATION NUMBER: 08/903,555
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/023,308
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/862,178
: PRIOR FILING DATE: May 22, 1997
```

```

: PRIOR APPLICATION NUMBER: 60/018,217
: PRIOR FILING DATE: May 23, 1996
: PRIOR APPLICATION NUMBER: 08/881,589
: PRIOR FILING DATE: June 24, 1997
: PRIOR APPLICATION NUMBER: 60/021,275
: PRIOR FILING DATE: June 25, 1996
: PRIOR APPLICATION NUMBER: 08/903,802
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/023,308
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/905,881
: PRIOR FILING DATE: August 1, 1997
: PRIOR APPLICATION NUMBER: 60/025,204
: PRIOR FILING DATE: August 1, 1996
: PRIOR APPLICATION NUMBER: 08/903,471
: PRIOR FILING DATE: July 30, 1997
: PRIOR APPLICATION NUMBER: 60/025,478
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/903,556
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/025,217
: PRIOR FILING DATE: August 22, 1996
: PRIOR APPLICATION NUMBER: 08/937,142
: PRIOR FILING DATE: September 23, 1997
: PRIOR APPLICATION NUMBER: 60/026,598
: PRIOR FILING DATE: September 24, 1996
: PRIOR APPLICATION NUMBER: 08/960,746
: PRIOR FILING DATE: October 29, 1997
: PRIOR APPLICATION NUMBER: 60/030,144
: PRIOR FILING DATE: October 30, 1996
: PRIOR APPLICATION NUMBER: 08/826,847
: PRIOR FILING DATE: April 10, 1997
: PRIOR APPLICATION NUMBER: 60/015,533
: PRIOR FILING DATE: April 10, 1996
: PRIOR APPLICATION NUMBER: 08/755,524
: PRIOR FILING DATE: November 22, 1996
: PRIOR APPLICATION NUMBER: 60/007,495
: PRIOR FILING DATE: November 22, 1995
: PRIOR APPLICATION NUMBER: 09/021,031
: PRIOR FILING DATE: February 10, 1998
: PRIOR APPLICATION NUMBER: 60/039,325
: PRIOR FILING DATE: February 13, 1997
: PRIOR APPLICATION NUMBER: 09/035,172
: PRIOR FILING DATE: March 4, 1998
: PRIOR APPLICATION NUMBER: 60/040,431
: PRIOR FILING DATE: March 5, 1997
: PRIOR APPLICATION NUMBER: 09/041,894
: PRIOR FILING DATE: March 12, 1998
: PRIOR APPLICATION NUMBER: 60/040,199
: PRIOR FILING DATE: March 14, 1997
: PRIOR APPLICATION NUMBER: 09/050,817
: PRIOR FILING DATE: March 30, 1998
: PRIOR APPLICATION NUMBER: 60/043,792
: PRIOR FILING DATE: April 11, 1997
: PRIOR APPLICATION NUMBER: 09/074,999
: PRIOR FILING DATE: May 8, 1998
: PRIOR APPLICATION NUMBER: 60/048,431
: PRIOR FILING DATE: May 29, 1997
: PRIOR APPLICATION NUMBER: 09/107,592
: PRIOR FILING DATE: June 30, 1998
: PRIOR APPLICATION NUMBER: 60/052,751
: PRIOR FILING DATE: July 1, 1997
: PRIOR APPLICATION NUMBER: 09/094,079
: PRIOR FILING DATE: June 9, 1998
: PRIOR APPLICATION NUMBER: 60/049,975
: PRIOR FILING DATE: June 13, 1997
: NUMBER OF SEQ ID NOS: 35654
: SOFTWARE: PERL Program
: SEQ ID NO 17019
: LENGTH: 295
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
```

; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00313702
; NAME/KEY: unsure
; LOCATION: 110, 172, 181, 202, 204, 223, 247, 249, 259-260, 263, 274, 293, 295
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-17019

Query Match 77.8%; Score 14; DB 5; Length 295;
Best Local Similarity 93.3%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 agtgcggtctcgct 18
||||||| |||||
Db 230 AGTGACGNTCTCGCT 216

Search completed: August 22, 2002, 00:50:53
Job time: 11893 sec

GenCorp version 4.5
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OW nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:50 ; Search time 2238.68 Seconds

(without alignments)
168.259 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18
Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: GenDbml:*
2: gb_ba:*
3: gb_htg:*
4: gb_in:*
5: gb_cm:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sts:*
13: gb_sy:*
14: gb_un:*
15: gb_vl:*
16: em_ba:*
17: em_fun:*
18: em_hum:*
19: em_in:*
20: em_mu:*
21: em_om:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
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1	18	100.0	335	8	AF162898	AF162898 Fusarium
2	18	100.0	335	8 <th>AF162899</th> <th>AF162899 Fusarium</th>	AF162899	AF162899 Fusarium
3	18	100.0	336	8 <th>AF162900</th> <th>AF162900 Fusarium</th>	AF162900	AF162900 Fusarium
4	18	100.0	455	8 <th>FOU28159</th> <th>U28159 Fusarium ox</th>	FOU28159	U28159 Fusarium ox
5	18	100.0	455	8 <th>FOU28161</th> <th>U28161 Fusarium ox</th>	FOU28161	U28161 Fusarium ox
6	18	100.0	456	8 <th>AF440527</th> <th>AF440527 Fusarium</th>	AF440527	AF440527 Fusarium
7	18	100.0	456	8 <th>AF440529</th> <th>AF440529 Fusarium</th>	AF440529	AF440529 Fusarium
8	18	100.0	456	8 <th>AF440531</th> <th>AF440531 Fusarium</th>	AF440531	AF440531 Fusarium
9	18	100.0	456	8 <th>AF440532</th> <th>AF440532 Fusarium</th>	AF440532	AF440532 Fusarium
10	18	100.0	456	8 <th>AF440534</th> <th>AF440534 Fusarium</th>	AF440534	AF440534 Fusarium
11	18	100.0	456	8 <th>AF440539</th> <th>AF440539 Fusarium</th>	AF440539	AF440539 Fusarium
12	18	100.0	456	8 <th>AF440540</th> <th>AF440540 Fusarium</th>	AF440540	AF440540 Fusarium
13	18	100.0	456	8 <th>AF440542</th> <th>AF440542 Fusarium</th>	AF440542	AF440542 Fusarium
14	18	100.0	456	8 <th>AF440552</th> <th>AF440552 Fusarium</th>	AF440552	AF440552 Fusarium
15	18	100.0	456	8 <th>AF440561</th> <th>AF440561 Fusarium</th>	AF440561	AF440561 Fusarium
16	18	100.0	456	8 <th>AF440563</th> <th>AF440563 Fusarium</th>	AF440563	AF440563 Fusarium
17	18	100.0	457	8 <th>AF440533</th> <th>AF440533 Fusarium</th>	AF440533	AF440533 Fusarium
18	18	100.0	457	8 <th>AF440538</th> <th>AF440538 Fusarium</th>	AF440538	AF440538 Fusarium
19	18	100.0	457	8 <th>AF440560</th> <th>AF440560 Fusarium</th>	AF440560	AF440560 Fusarium
20	18	100.0	457	8 <th>AF440562</th> <th>AF440562 Fusarium</th>	AF440562	AF440562 Fusarium
21	18	100.0	458	8 <th>AF055220</th> <th>AF055220 Fusarium</th>	AF055220	AF055220 Fusarium
22	18	100.0	506	8 <th>AF069310</th> <th>AF069310 Fusarium</th>	AF069310	AF069310 Fusarium
23	18	100.0	520	8 <th>FOU34566</th> <th>U34566 Fusarium ox</th>	FOU34566	U34566 Fusarium ox
24	18	100.0	521	8 <th>AF176656</th> <th>AF176656 Fusarium</th>	AF176656	AF176656 Fusarium
25	18	100.0	531	8 <th>AF242876</th> <th>AF242876 Fusarium</th>	AF242876	AF242876 Fusarium
26	18	100.0	544	8 <th>FOXYRNA</th> <th>X94173 Fusarium ox</th>	FOXYRNA	X94173 Fusarium ox
27	18	100.0	545	8 <th>FOYBIE58</th> <th>X78260 F.oxysporum</th>	FOYBIE58	X78260 F.oxysporum
28	18	100.0	546	8 <th>FOYCB58</th> <th>X78259 F.oxysporum</th>	FOYCB58	X78259 F.oxysporum
29	18	100.0	546	8 <th>FOYCN58</th> <th>X78258 F.oxysporum</th>	FOYCN58	X78258 F.oxysporum
30	18	100.0	616	8 <th>AF322074</th> <th>AF322074 Fusarium</th>	AF322074	AF322074 Fusarium
31	18	100.0	616	8 <th>AF322075</th> <th>AF322075 Fusarium</th>	AF322075	AF322075 Fusarium
32	18	100.0	616	8 <th>AF322076</th> <th>AF322076 Fusarium</th>	AF322076	AF322076 Fusarium
33	18	100.0	636	8 <th>AF443071</th> <th>AF443071 Fusarium</th>	AF443071	AF443071 Fusarium
34	18	100.0	1471	8 <th>FO58BRNA</th> <th>Y07991 F.oxysporum</th>	FO58BRNA	Y07991 F.oxysporum
35	16.4	91.1	456	8 <th>AF132799</th> <th>AF132799 Fusarium</th>	AF132799	AF132799 Fusarium
36	16.4	91.1	456	8 <th>AF440525</th> <th>AF440525 Fusarium</th>	AF440525	AF440525 Fusarium
37	16.4	91.1	456	8 <th>AF440526</th> <th>AF440526 Fusarium</th>	AF440526	AF440526 Fusarium
38	16.4	91.1	456	8 <th>AF440527</th> <th>AF440527 Fusarium</th>	AF440527	AF440527 Fusarium
39	16.4	91.1	456	8 <th>AF440535</th> <th>AF440535 Fusarium</th>	AF440535	AF440535 Fusarium
40	16.4	91.1	456	8 <th>AF440536</th> <th>AF440536 Fusarium</th>	AF440536	AF440536 Fusarium
41	16.4	91.1	456	8 <th>AF440537</th> <th>AF440537 Fusarium</th>	AF440537	AF440537 Fusarium
42	16.4	91.1	456	8 <th>AF440541</th> <th>AF440541 Fusarium</th>	AF440541	AF440541 Fusarium
43	16.4	91.1	456	8 <th>AF440544</th> <th>AF440544 Fusarium</th>	AF440544	AF440544 Fusarium
44	16.4	91.1	456	8 <th>AF440545</th> <th>AF440545 Fusarium</th>	AF440545	AF440545 Fusarium
45	16.4	91.1	456	8 <th>AF440546</th> <th>AF440546 Fusarium</th>	AF440546	AF440546 Fusarium
					AF440547	Fusarium

ALIGNMENTS

RESULT 1
AF162898
LOCUS
DEFINITION
Fusarium oxysporum f. sp. congluticans 335 bp DNA linear PLN 15-NOV-2001
Partial sequence: Internal transcribed spacer 2, complete sequence:
and 28S ribosomal RNA gene, partial sequence.

ACCESSION
AF162898
AF162898.1 GI:5690387

VERSION
AF162898.1

KEYWORDS
Fusarium oxysporum f. sp. congluticans.
Fusarium oxysporum f. sp. congluticans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.

ORGANISM
Fusarium oxysporum f. sp. congluticans.
Fusarium oxysporum f. sp. congluticans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.

REFERENCE
1 (bases 1 to 335)
Min.B.R.
Direct Submission
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea

JOURNAL
Location/Qualifiers

FEATURES
1..335
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/strain="MAFF 744001"

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/db_xref="taxon:100902"
/feature="forma specialis: congluticans"
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129..277
/product="internal transcribed spacer 2"
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 335;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgtaattcgctctc 18
|||||
Db 162 CGTTAATTCGCTTCCTC 179

RESULT 2
AF162899 335 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION
Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene,
partial sequence; internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence.
AF162899
VERSION
AF162899.1 GI:5690388
KEYWORDS
SOURCE
Fusarium oxysporum f. sp. fragariae.
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
1 (bases 1 to 335)
REFERENCE
1 (bases 1 to 335)
AUTHORS
Min, B.R.
TITLE
Direct Submission
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL
FEATURES
Source
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/organism="Fusarium oxysporum f. sp. fragariae"
/strain="MAF 744009"
/db_xref="taxon:100903"
/note="forma specialis: fragariae"
<1..128
/product="5.8S ribosomal RNA"
129..277
/product="internal transcribed spacer 2"
278..>335
/product="28S ribosomal RNA"
88 a 81 c 82 g 84 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 335;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgtaattcgctctc 18
|||||
Db 162 CGTTAATTCGCTTCCTC 179

RESULT 3
AF162900 336 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION
Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial
sequence; internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
AF162900
VERSION
AF162900.1 GI:5690389

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KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum f. sp. raphani.
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
1 (bases 1 to 336)
REFERENCE
1 (bases 1 to 336)
AUTHORS
Min, B.R.
TITLE
Direct Submission
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL
FEATURES
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/organism="Fusarium oxysporum f. sp. raphani"
/db_xref="taxon:96318"
/note="forma specialis: raphani"
<1..128
/product="5.8S ribosomal RNA"
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/product="internal transcribed spacer 2"
275..>336
/product="28S ribosomal RNA"
89 a 81 c 82 g 84 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 336;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgtaattcgctctc 18
|||||
Db 163 CGTTAATTCGCTTCCTC 180

RESULT 4
F0028159 455 bp DNA linear PLN 08-JUN-1995
LOCUS
DEFINITION
Fusarium oxysporum strain DAOM 213391 internal transcribed spacer
region ITS1, 5.8S ribosomal RNA gene, and internal transcribed
spacer region ITS2. Includes the 5.8S gene.
F0028159
VERSION
U28159.1 GI:852527
KEYWORDS
SOURCE
Fusarium oxysporum.
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
1 (bases 1 to 455)
REFERENCE
1 (bases 1 to 455)
AUTHORS
Duggal, A.
TITLE
Direct Submission
Submitted (31-MAY-1995) Artie Duggal, Forestry, University of
Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada
JOURNAL
FEATURES
Source
1..455
/organism="Fusarium oxysporum"
/strain="DAOM 213391"
/db_xref="taxon:5507"
/note="The fungus was determined by Selfert K.A. and was
isolated from wilted carnations from Kenya by Tewari J.P."
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/note="internal transcribed spacer region; ITS1"
148..304
/product="5.8S ribosomal RNA"
305..455
/note="internal transcribed spacer region; ITS2"
119 a 122 c 100 g 114 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 455;

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Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||||||
 Db 338 CGTTAATTCCGCTTCCTC 355

RESULT 5
 FOU28161 455 bp DNA linear PLN 08-JUN-1995
 LOCUS FOU28161
 DEFINITION Fusarium oxysporum strain CBS 171.31 internal transcribed spacer
 region ITS1, 5.8S ribosomal RNA gene, and internal transcribed
 spacer region ITS2. Includes the 5.8S gene.

ACCESSION U28161
 VERSION U28161.1 GI:852529
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 455)
 AUTHORS Duggal, A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-1995) Artie Duggal, Forestry, University of
 Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada

FEATURES
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 1..455
 /organism="Fusarium oxysporum"
 /strain="CBS 171.31"
 /db_xref="taxon:5507"
 /note="The fungus was isolated and identified by
 Wollenweber H.W. from Pinus sp. from Germany"
 1..147
 /note="Internal transcribed spacer region; ITS1"
 148..304
 /product="5.8S ribosomal RNA"
 305..455
 /note="Internal transcribed spacer region; ITS2"
 120 a 122 c 99 g 114 t

BASE COUNT 120 a 122 c 99 g 114 t

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 455;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||||||
 Db 338 CGTTAATTCCGCTTCCTC 355

RESULT 6
 AF440527 456 bp DNA linear PLN 02-JAN-2002
 LOCUS AF440527
 DEFINITION Fusarium oxysporum isolate 14RK-11 internal transcribed spacer 1,
 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
 complete sequence.

ACCESSION AF440527
 VERSION AF440527.1 GI:18034395
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
 from tomato plants
 JOURNAL Can. J. Bot. (2002) In press
 REFERENCE 2 (bases 1 to 456) In press
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.

TITLE Direct Submission
 JOURNAL Submitted (23-Oct-2001) Vegetable Laboratory, USDA-ARS, 10300
 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 /product="Internal transcribed spacer 1"
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 306..456
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BASE COUNT 120 a 124 c 99 g 113 t

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||||||
 Db 339 CGTTAATTCCGCTTCCTC 356

RESULT 7
 AF440529 456 bp DNA linear PLN 02-JAN-2002
 LOCUS AF440529
 DEFINITION Fusarium oxysporum isolate 35RK-14 internal transcribed spacer 1,
 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
 complete sequence.

ACCESSION AF440529
 VERSION AF440529.1 GI:18034397
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
 from tomato plants
 JOURNAL Can. J. Bot. (2002) In press
 REFERENCE 2 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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 306..456
 /product="Internal transcribed spacer 2"
 120 a 124 c 99 g 113 t

BASE COUNT 120 a 124 c 99 g 113 t

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||||||
 Db 339 CGTTAATTCCGCTTCCTC 356

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RESULT 8
AF440531 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440531
DEFINITION Fusarium oxysporum isolate 44RK-35 internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF440531
VERSION AF440531.1 GI:18034399
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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/product="Internal transcribed spacer 1"
rRNA 148..305
/product="5.8S ribosomal RNA"
misc_RNA 306..456
/product="Internal transcribed spacer 2"
BASE COUNT 120 a 124 c 99 g 113 t
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Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgttaatcgcttcctc 18
|||||
DB 339 CGTTAATTCGCGTTCCTC 356

RESULT 9
AF440532 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440532
DEFINITION Fusarium oxysporum isolate 73RK-1 internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF440532
VERSION AF440532.1 GI:18034400
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

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FEATURES
source Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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/product="Internal transcribed spacer 1"
rRNA 148..305
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misc_RNA 306..456
/product="Internal transcribed spacer 2"
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgttaatcgcttcctc 18
|||||
DB 339 CGTTAATTCGCGTTCCTC 356

RESULT 10
AF440534 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440534
DEFINITION Fusarium oxysporum isolate AL22 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440534
VERSION AF440534.1 GI:18034402
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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misc_RNA 1..147
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rRNA 148..305
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misc_RNA 306..456
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BASE COUNT 120 a 124 c 99 g 113 t
ORIGIN
Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgttaatcgcttcctc 18
|||||
DB 339 CGTTAATTCGCGTTCCTC 356

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RESULT 11
AF440539 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440539
DEFINITION Fusarium oxysporum isolate DEH1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440539
VERSION AF440539.1 GI:18034407
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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1. .456
/organism="Fusarium oxysporum"
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/db_xref="taxon:5507"
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1. .147
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rRNA
148. .305
/product="5.8S ribosomal RNA"
misc_RNA
306. .456
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BASE COUNT 120 a 124 c 99 g 113 t
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 cgtaatcgcgttcctc 18
|||||
Db 339 CGTTAATTCGCGTTCCTC 356
RESULT 12
AF440540 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440540
DEFINITION Fusarium oxysporum isolate DEH2 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440540
VERSION AF440540.1 GI:18034408
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
Location/Qualifiers

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/db_xref="taxon:5507"
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148. .305
/product="5.8S ribosomal RNA"
misc_RNA
306. .456
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BASE COUNT 120 a 124 c 99 g 113 t
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 cgtaatcgcgttcctc 18
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Db 339 CGTTAATTCGCGTTCCTC 356
RESULT 13
AF440542 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440542
DEFINITION Fusarium oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440542
VERSION AF440542.1 GI:18034410
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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148. .305
/product="5.8S ribosomal RNA"
misc_RNA
306. .456
/product="Internal transcribed spacer 2"
BASE COUNT 120 a 124 c 99 g 113 t
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Query Match 100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 cgtaatcgcgttcctc 18
|||||
Db 339 CGTTAATTCGCGTTCCTC 356
RESULT 14
AF440552

```

LOCUS      AF440552          456 bp    DNA     linear     PLN 02-JAN-2002
DEFINITION Fusarium oxysporum isolate IA7 Internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence.
ACCESSION  AF440552
VERSION    AF440552.1  GI:18034420
KEYWORDS
SOURCE
ORGANISM   Fusarium oxysporum.
            Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 456)
            Bao,J.R., Fravel,D.R. and Lazarovits,G.
            Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
            from tomato plants
            Can. J. Bot. (2002) In press
REFERENCE  2 (bases 1 to 456)
            Bao,J.R., Fravel,D.R. and Lazarovits,G.
            Direct Submission
            Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
            Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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               /product="Internal transcribed spacer 2"
BASE COUNT 120 a 124 c 99 g 113 t
ORIGIN
Query Match          100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgttaatcgagtcctc 18
    |||
Db 339 CGTTAATCGCGTTCCTC 356

RESULT 15
AF440561          456 bp    DNA     linear     PLN 02-JAN-2002
LOCUS      AF440561
DEFINITION Fusarium oxysporum isolate PE11 Internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence.
ACCESSION  AF440561
VERSION    AF440561.1  GI:18034429
KEYWORDS
SOURCE
ORGANISM   Fusarium oxysporum.
            Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE  1 (bases 1 to 456)
            Bao,J.R., Fravel,D.R. and Lazarovits,G.
            Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
            from tomato plants
            Can. J. Bot. (2002) In press
REFERENCE  2 (bases 1 to 456)
            Bao,J.R., Fravel,D.R. and Lazarovits,G.
            Direct Submission
            Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
            Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
            source
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               /organism="Fusarium oxysporum"

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            148..305
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            306..456
               /product="Internal transcribed spacer 2"
BASE COUNT 120 a 124 c 99 g 113 t
ORIGIN
Query Match          100.0%; Score 18; DB 8; Length 456;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cgttaatcgagtcctc 18
    |||
Db 339 CGTTAATCGCGTTCCTC 356

Search completed: August 21, 2002, 22:09:51
Job time: 14205 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using 4w model

Run on: August 21, 2002, 22:22:44 ; Search time 594.49 Seconds
(without alignments)
51.985 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18
Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	18	100.0	18	20	AAV83697	Species-specific P
2	18	100.0	382	21	AAV72783	5.8S rRNA gene seq
C 3	15	83.3	128	23	AA548419	Enterococcus faeca
C 4	15	83.3	250	23	AA547978	Enterococcus faeca
C 5	15	83.3	9212	20	AAV13271	Enterococcus faeca
6	14.8	82.2	650	22	AA505503	Mammalian vestibul
7	14.8	82.2	1200	23	AB112625	Drosophila melanog
C 8	14.8	82.2	3138	23	AA552883	Enterococcus faeca
C 9	14.8	82.2	3257	23	AB112624	Drosophila melanog

10	14.8	82.2	4491	23	ABL02050	Drosophila melanog
11	14.8	82.2	5864	23	ABL03754	Drosophila melanog
12	14.8	82.2	15428	23	ABL02692	Drosophila melanog
13	14.4	80.0	939	22	AAH53833	S. epidermidis ope
14	14.4	80.0	2815	22	AAH54455	S. epidermidis gen
15	14	77.8	3208	15	AA071481	omp2 locus of Bruc
16	14	77.8	3345	15	AA071485	omp2 locus of Bruc
17	14	77.8	3346	15	AA071483	omp2 locus of Bruc
18	14	77.8	3347	15	AA071486	omp2 locus of Bruc
19	14	77.8	3347	15	AA071480	omp2 locus of Bruc
20	14	77.8	3361	15	AA071484	omp2 locus of Bruc
21	14	77.8	3436	15	AA064597	Drosophila melanog
22	14	77.8	20629	23	ABL09022	Rice centeromeric
23	13.8	76.7	701	22	AAV28160	Arabidopsis thaila
24	13.8	76.7	882	22	AAV33415	Human EST-derived
25	13.8	76.7	886	22	AAH98792	Human tumour suppr
26	13.8	76.7	1076	22	AAH23689	Aspergillus oryzae
27	13.8	76.7	1215	17	AAV13122	AcNPV ORF 62, res1
28	13.8	76.7	1551	21	AAV13666	Human immune syste
29	13.8	76.7	2701	24	ABL34324	cDNA encoding Dros
30	13.8	76.7	5167	22	AAV57189	Drosophila melanog
31	13.8	76.7	5167	23	ABL27091	Helper plasmid 3E1
32	13.8	76.7	5679	22	AAV58502	Human immune syste
33	13.8	76.7	6301	22	ABL35052	Virulence gene 441
34	13.8	76.7	6642	21	AAV79621	Plasmid p3E1.2 con
35	13.8	76.7	6723	22	AAV85592	p15p70/opd plasmid
36	13.8	76.7	6723	22	AAV85593	Plasmid p3E1.2hs/o
37	13.8	76.7	7560	22	AAV85599	Nucleotide sequenc
38	13.8	76.7	9423	22	AAV55577	Photorehabdus lumin
39	13.8	76.7	9717	20	AAV06826	Potato pollen cell
40	13.8	76.7	10811	19	AAV59091	Streptococcus pneu
41	13.8	76.7	12666	19	AAV52270	Human reproductive
42	13.8	76.7	13046	22	AAV03250	Human DNA for a no
43	13.8	76.7	13046	22	AAV31516	DNA encoding Dros
44	13.8	76.7	17847	22	AAV57188	Drosophila melanog
45	13.8	76.7	17847	23	ABL27090	

ALIGNMENTS

RESULT 1

AAV83697 standard; DNA: 18 BP.

AAV83697:

26-FEB-1999 (first entry)

Species-specific probe targeted to the internal transcribed spacer 2.

Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
 Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
 Penicillium notatum; Sporotrich schenckii; filamentous fungus; ss.

Synthetic.
Fusarium oxysporum.

Key modified_base 1 Location/Qualifiers
/tag= a
/note= "labelled with digoxigenin"

W09850584-AZ.

12-NOV-1998.

01-MAY-1998; 98MO-US08926.

```
PR 02-MAY-1997: 97US-0045400.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
PI Aldorevich L, Chol JS, Morrison CJ, Reiss E;
XX
XX WPI; 1999-034737/03.
DR
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
XX Example 1; Page 22; 45pp; English.
PS
XX
XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
CC nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
CC plumbeus, M. indicus, M. circinelloides f. circinelloides, Rhizopus
CC oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor
CC pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
CC boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
XX Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgttaatcgcttcctc 18
1 |||||||||
Db 1 cgttaatcgcttcctc 18

RESULT 2
AAAT2783
ID AAAT2783 standard; DNA: 382 BP.
XX
XX AAAT2783:
AC
AC 13-DEC-2000 (first entry)
DT
XX
XX 5.8s rRNA gene sequence.
DE
XX
XX Black spot disease; brown spot disease; fungi; fruit vegetable;
KW field crop; Alternaria; 5.8s rRNA; detection; ds.
XX
XX Fusarium oxysporum.
OS
XX
XX WO200046397-A1.
PM
XX
XX 10-AUG-2000.
PD
XX
XX 24-JAN-2000; 2000WO-US01466.
PE
XX
XX 02-FEB-1999; 99US-0241427.
PR
XX
XX (TECR ) TECHNION RES & DEV FOUND LTD.
PA (KASH/) KASHI Y.
XX
XX Kashi Y, Zur G, Sharf R, Hallerman E;
PI
XX
XX WPI; 2000-499381/44.
DR
XX
XX Nucleic acid based assay and kit for detection of Alternaria
PT contamination in food products involves analysing the sample of food
PT product for nucleic acid sequences unique to Alternaria -
```

```
XX
XX Examples; Fig 1; 47pp; English.
PS
XX
XX The invention relates to a nucleic acid based method for the detection
CC of Alternaria contamination in a food product. The method involves
CC obtaining and analysing a food product sample for a nucleic acid sequence
CC unique to Alternaria. Detectable levels of the nucleic acid sequence can
CC be used as an indication of Alternaria contamination. Fungi from the
CC genus Alternaria are ubiquitous saprophytes and are economically
CC important pathogens affecting a wide range of plants. Alternaria are the
CC causative agents of black or brown spot disease in many fruits,
CC vegetables and field crops. The method is used for the detection of
CC Alternaria contamination in food products. The present sequence
CC represents the Fusarium oxysporum 5.8s rRNA gene, used in examples
CC illustrating the invention.
XX
XX Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 18; DB 21; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgttaatcgcttcctc 18
1 |||||||||
Db 287 cgttaatcgcttcctc 304

RESULT 3
AAS48419/C
ID AAS48419 standard; DNA: 128 BP.
XX
XX AAS48419;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Enterococcus faecalis cellular proliferation inhibitory sequence #989.
DE
XX
XX Antisense; ss; prokaryotic cellular proliferation;
KW antibiotic; antibacterial; drug design.
XX
XX Enterococcus faecalis.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PF
XX
XX 21-MAR-2000; 2000US-191078P.
PR
XX
XX 23-MAY-2000; 2000US-206848P.
PR
XX
XX 26-MAY-2000; 2000US-207727P.
PR
XX
XX 23-OCT-2000; 2000US-242578P.
PR
XX
XX 27-NOV-2000; 2000US-253625P.
PR
XX
XX 22-DEC-2000; 2000US-257931P.
PR
XX
XX 16-FEB-2001; 2001US-269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
XX Claim 1; Seq ID No 996; 51pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
```

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence is an antisense
CC oligonucleotide of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 other;

Query Match 83.3%; Score 15; DB 23; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaaatcgcgctcc 16
|||||
DB 118 GTTAATTGCGGTCC 104

RESULT 4

AA547978/c
ID AA547978 standard; DNA; 250 BP.

AC AA547978;

DT 13-FEB-2002 (first entry)

DE *Enterococcus faecalis* cellular proliferation inhibitory sequence #548.

XX
XX Antisense; ss; prokaryotic cellular proliferation;
XX antibiotic; antibacterial; drug design.

OS *Enterococcus faecalis*.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX
XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI: 2001-611495/70.

XX
XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX
XX Claim 1; Seq ID No 555; 511pp; English.

XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence is an antisense
CC oligonucleotide of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 other;

Query Match 83.3%; Score 15; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaaatcgcgctcc 16
|||||
DB 54 GTTAATTGCGGTCC 40

RESULT 5

AA13271
ID AA13271 standard; DNA; 9212 BP.

AC AA13271;

DT 19-MAR-1999 (first entry)

DE *Enterococcus faecalis* genome contig SEQ ID NO:334.

XX
XX *Enterococcus faecalis*; contig; detection; *Enterococcal* infection;
XX vaccine; attenuation; computer readable medium; ds.

OS *Enterococcus faecalis*.

PN WO9850555-A2.

PD 12-NOV-1998.

PF 04-MAY-1998; 98WO-US08985.

PR 14-NOV-1997; 97US-0066009.

PR 06-MAY-1997; 97US-0044031.

PR 16-MAY-1997; 97US-0046655.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Dillon PJ, Kunsch CA;

XX WPI: 1999-045171/04.

XX
XX New isolated *Enterococcus faecalis* polynucleotides and polypeptides

PT - used to develop products for the detection of *Enterococcus* and for

PT use in vaccines for prevention or attenuation of *Enterococcus*

PT infection.
XX
XX Claim 1; Page 1436-1441; 2084pp; English.

XX
XX A computer readable medium has been developed which has recorded on it

XX 982 nucleotide sequences isolated from the *Enterococcus faecalis* genome.
CC AA12938 to AA13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the *Enterococcus faecalis* genome with
CC commercial importance. The products can be used to detect the presence
CC of *Enterococcus faecalis* in samples. They can also be used for

diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection.

Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 13 other;

Query Match 83.3%; Score 15; DB 20; Length 9212;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 gctaatcgcttc 16
|||||
Db 4989 gctaatcgcttc 5003

RESULT 6

AAS05503 standard; DNA; 650 BP.

AAS05503;

07-SEP-2001 (first entry)

Mammalian vestibular system geotactic behaviour modulator gene #103.

Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo; graviperceptive disorder; motion sickness; labyrinthitis; sypnalls; ds; Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy; trauma; infection of the middle ear; ototoxic agent exposure.

Drosophila melanogaster .

WO200140519-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32639.

02-DEC-1999; 99US-0168579.

26-SEP-2000; 2000US-0669751.

(NEUR-) NEUROSCIENCES RES FOUND INC.

Greenspan RJ;

WPI; 2001-356159/37.

New isolated nucleic acid having mammalian vestibular system-modulating activity useful in the treatment of disorders such as motion sickness and vertigo .

Claim 59; Page 126; 179pp; English.

The sequences shown in AAS05401-AAS0561 represent DNA with mammalian vestibular system-modulating activity. The DNA sequences can be used in a method whereby a first and second strain of an invertebrate is obtained, and both are subjected to conditions in which the strains exhibit different geotactic behaviour. Genes that are differentially expressed in the first strain relative to the second strain are then identified. Mammalian genes having substantially the same nucleic acid sequence as these genes are used to decrease the symptoms of graviperceptive disorders such as motion sickness, vertigo, labyrinthitis, Meniere's disease, acoustic neuroma, multiple sclerosis, sypnalls, trauma, infection of the middle ear, exposure to ototoxic agents and epilepsy.

Sequence 650 BP; 182 A; 181 C; 167 G; 120 T; 0 other;

Query Match 82.2%; Score 14.8; DB 22; Length 650;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cgtaatcgcttc 18
|||||
Db 69 cgtcatacgcttc 86

RESULT 7

ABL12625 standard; cDNA; 1200 BP.

ABL12625;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 32357.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PMD, Myers EW;

WPI; 2001-656860/75.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 32357; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pcl_sequences.

Sequence 1200 BP; 335 A; 319 C; 318 G; 228 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 1200;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cgtaatcgcttc 18
|||||
Db 75 cgtcatacgcttc 92

RESULT 8

AAS52883/c

ID AAS52883 standard; DNA; 3138 BP.
XX
AC AAS52883;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis DNA for cellular proliferation protein #311.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
XX antibiotic; antibacterial; drug design.
OS
XX Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
XX
PR 23-MAY-2000; 2000US-206848P.
XX
PR 26-MAY-2000; 2000US-207727P.
XX
PR 23-OCT-2000; 2000US-242578P.
XX
PR 27-NOV-2000; 2000US-253625P.
XX
PR 22-DEC-2000; 2000US-257931P.
XX
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
DR P-PSDB: AA035024.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 6520; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3138 BP; 1239 A; 554 C; 631 G; 714 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 3138;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||
DB 1644 CGTAAATCCGCTTCGC 1627

RESULT 9

ABL12624/C
ID ABL12624 standard; cDNA; 3257 BP.
XX
AC ABL12624;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32354.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-656860/75.
DR P-PSDB: ABB68521.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 32354; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
CC sequences (ABB5737-ABB72072),
CC (ABB5737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3257 BP; 796 A; 793 C; 717 G; 951 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 3257;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||
DB 2183 CGTTCATACGCGTTCCTC 2166

RESULT 10
ID ABL02050 standard; cDNA; 4491 BP.
XX
AC ABL02050;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 632.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX

OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB57947.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 637; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB16175) and the encoded DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 4491 BP; 1161 A; 1000 C; 969 G; 1361 T; 0 other;
 XX

Query Match 82.2%; Score 14.8; DB 23; Length 4491;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaatcgcgtcttc 18
 ||||||||| || |||||
 Db 760 cgttaatcgcgtcttc 777

RESULT 11
 ABL03754
 ID ABL03754 standard; cDNA; 5864 BP.
 XX
 AC ABL03754;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5744.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PA WO200171042-A2.
 XX
 PI 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX

XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB59651.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 5744; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB16175) and the encoded DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 5864 BP; 1530 A; 1320 C; 1262 G; 1752 T; 0 other;
 XX

Query Match 82.2%; Score 14.8; DB 23; Length 5864;
 Best Local Similarity 78.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaatcgcgtcttc 18
 ||||||||| || |||||
 Db 4942 cgttaatcgcgtcttc 4959

RESULT 12
 ABL02692
 ID ABL02692 standard; cDNA; 15428 BP.
 XX
 AC ABL02692;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2558.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PA WO200171042-A2.
 XX
 PI 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB58589.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 2558; 21pp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB85737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.
CC
CC
SQ Sequence 15428 BP; 4834 A; 2815 C; 2869 G; 4910 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 15428;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||||
DB 8063 cgttaatcacttcctc 8080

RESULT 13
AAH53833/C
ID AAH53833 standard; DNA: 939 BP.

AC AAH53833;

DT 03-SEP-2001 (first entry)

DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3059.

KM *Staphylococcus epidermidis* SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.

OS *Staphylococcus epidermidis*.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000MO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI *Kimmerly MJ*;

PT WPI: 2001-316495/33.

DR P-PSDB: AAG82983.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 805; 2188bp; English.

AAH5304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to
CC AAH5098 represent oligonucleotide sequences and primers which are used

CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
CC
SQ Sequence 939 BP; 322 A; 122 C; 183 G; 312 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 939;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ttaatcgcttcctc 18
|||||||
DB 616 ttaatcagcttcctc 601

RESULT 14
AAH54455
ID AAH54455 standard; DNA: 2815 BP.

AC AAH54455;

DT 03-SEP-2001 (first entry)

DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3819.

KM *Staphylococcus epidermidis* SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.

OS *Staphylococcus epidermidis*.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000MO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI *Kimmerly MJ*;

PT WPI: 2001-316495/33.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 1457-1458; 2188bp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to
CC AAH5098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.

XX
SQ Sequence 2815 BP; 958 A; 518 C; 315 G; 1024 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 2815;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ttaattcgcttcctc 18
|||||
DB 792 ttaattcgcttcctc 807

RESULT 15

AA071481/C
ID AA071481 standard; cDNA; 3208 BP.

AC AA071481;

DT 01-MAY-1995 (first entry)

DE omp2 locus of Brucella abortus biovar 1 (S2308).

KW omp2; consensus; Brucella; identification; diagnosis; infection;
KW biovar; cattle; disease; ss.

OS Brucella abortus biovar 1 (S2308).

PN US5348857-A.

PD 20-SEP-1994.

PF 22-MAY-1990; 90US-0527017.

PR 22-MAY-1990; 90US-0527017.

XX 06-NOV-1992; 92US-0972791.

PA (TEXA) UNIV TEXAS A & M.

PI Adams LG, Ficht TA;

DR WPI: 1994-302203/37.

PT Identification of Brucella species or biovars - by amplification
of the Brucella omp2 gene locus and hybridisation with DNA probes

PS Disclosure; Columns 17-21; 50pp; English.

CC Rapid detection of Brucella may be achieved by amplifying the omp2
gene locus of Brucella (which shows genetic variation correlating
with established species designations) and hybridising the amplified
sequence with a panel of DNA probes to identify a species of biovar
of Brucella. The amplified sequence is preferably a sequence between
CC nucleotides 2470 and 3346 of the consensus sequence described in
AA071479. The method is used for the detection of Brucella infection in
CC animals, particularly humans and cattle.
XX

SO Sequence 3208 BP; 761 A; 864 C; 868 G; 715 T; 0 other;

Query Match 77.8%; Score 14; DB 15; Length 3208;
Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
|||||
DB 1488 gtaattcgcttc 1475

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:12:29 ; Search time 138.45 Seconds

(without alignments)
31.935 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcttcctc 18

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCUTS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	77.8	3208	1	US-07-972-791-3 Sequence 3, Appl1
2	14	77.8	3345	1	US-07-972-791-7 Sequence 7, Appl1
3	14	77.8	3346	1	US-07-972-791-5 Sequence 5, Appl1
4	14	77.8	3347	1	US-07-972-791-2 Sequence 2, Appl1
5	14	77.8	3347	1	US-07-972-791-8 Sequence 8, Appl1
6	14	77.8	3361	1	US-07-972-791-6 Sequence 6, Appl1
7	14	77.8	3434	6	5310649-1 Patent No. 5310649
8	13	76.7	5679	4	US-08-844-274-10 Sequence 10, Appl1
9	13	76.7	6723	4	US-08-844-274-13 Sequence 13, Appl1
10	13	76.7	6723	4	US-08-844-274-14 Sequence 14, Appl1
11	13	76.7	7560	4	US-08-844-274-20 Sequence 20, Appl1
12	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
13	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
14	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
15	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
16	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
17	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
18	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
19	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
20	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
21	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
22	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
23	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
24	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
25	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
26	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1
27	13	76.7	9717	4	US-09-251-645-1 Sequence 1, Appl1

C 28	12.8	71.1	1977	4	US-09-626-589-5	Sequence 5, Appl1
C 29	12.8	71.1	2151	4	US-09-626-589-4	Sequence 4, Appl1
C 30	12.8	71.1	2185	1	US-08-173-508-3	Sequence 3, Appl1
C 31	12.8	71.1	2185	2	US-08-265-310-3	Sequence 3, Appl1
C 32	12.8	71.1	2185	3	US-08-951-742-3	Sequence 3, Appl1
C 33	12.8	71.1	2346	1	US-08-724-298A-1	Sequence 1, Appl1
C 34	12.8	71.1	2472	4	US-09-626-589-6	Sequence 6, Appl1
C 35	12.8	71.1	4379	1	US-08-592-214A-17	Sequence 17, Appl1
C 36	12.8	71.1	4379	3	US-09-149-976-17	Sequence 1, Appl1
C 37	12.8	71.1	5163	3	US-08-700-651-1	Sequence 1, Appl1
C 38	12.8	71.1	5163	3	US-08-928-361B-4	Sequence 4, Appl1
C 39	12.8	71.1	5318	3	US-08-700-651-2	Sequence 2, Appl1
C 40	12.8	71.1	5318	3	US-08-928-361B-3	Sequence 3, Appl1
C 41	12.8	71.1	5511	3	US-08-928-361B-2	Sequence 2, Appl1
C 42	12.8	71.1	7334	3	US-08-928-361B-1	Sequence 1, Appl1
C 43	12.4	68.9	4249	1	US-08-480-784-21	Sequence 21, Appl1
C 44	12.4	68.9	4249	1	US-08-483-553-21	Sequence 21, Appl1
C 45	12.4	68.9	4249	1	US-08-487-002-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-07-972-791-3/C
Sequence 3, Application US/07972791
Patent No. 5318657
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: PRAYEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3208 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
SPRAIN: biovar 1 (S2308)
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcggttc 15
DB 1488 GTTAATTCGCGTTC 1475

RESULT 2

US-07-972-791-7/C
Sequence 7, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972.791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3345 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella melitensis
STRAIN: biovar 1
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 gtaattcggttc 15
DB 1487 GTTAATTCGCGTTC 1474

RESULT 3

US-07-972-791-5/C
Sequence 5, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER

STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972.791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3346 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella neotomae
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 gtaattcggttc 15
DB 1488 GTTAATTCGCGTTC 1475

RESULT 4

US-07-972-791-2/C
Sequence 2, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972.791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165

TELEX: 792026
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 5
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
DB 1488 GTTAATTCGCTTC 1475

RESULT 5
US-07-972-791-8/c
Sequence 8, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella suis
STRAIN: biovar 1
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
DB 1488 GTTAATTCGCTTC 1475

RESULT 6
US-07-972-791-6/c
Sequence 6, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3361 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella ovis
US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
DB 1503 GTTAATTCGCTTC 1490

RESULT 7
5310649-1/c
Patent No. 5310649
APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, L. Gary
TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS
OF BRUCELLA
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/527,017
FILING DATE: 22-MAY-1990
SEQ ID NO: 1;
LENGTH: 3434
5310649-1

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: RESULT 9
: US-08-844-274-13/C
: Sequence 13, Application US/08844274B
: Patent No. 6218185
: GENERAL INFORMATION:
: APPLICANT: Fraser Jr., Malcom J.
: APPLICANT: Shirk, Paul D.
: APPLICANT: Ellick, Teri A.
: APPLICANT: Perera, Omachage
: TITLE OF INVENTION: Piggybac Transposon-Based Genetic Transformation S
: TITLE OF INVENTION: for insects
: FILE REFERENCE: 0148.36
: CURRENT APPLICATION NUMBER: US/08/844,274B
: CURRENT FILING DATE: 1997-04-18
: EARLIER APPLICATION NUMBER: 60/016,234
: EARLIER FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO 13
: LENGTH: 6723
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Clone p3el.2H/S
: US-08-844-274-13

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RESULT 11
US-08-844-274-20
: Sequence 20. Application US/08844274B
: Patent No. 6218185
: GENERAL INFORMATION:
: APPLICANT: Fraser Jr., Malcom J.
: APPLICANT: Shirk, Paul D.
: APPLICANT: Ellick, Teri A.
: APPLICANT: Pereira, Omachage
: TITLE OF INVENTION: Piggybac Transposon-Based Genetic Transformation System
: TITLE OF INVENTION: for insects
: FILE REFERENCE: 0148.96
: CURRENT APPLICATION NUMBER: US/08/844.274B
: CURRENT FILING DATE: 1997-04-18
: EARLIER APPLICATION NUMBER: 60/016.234
: EARLIER FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO 20
: LENGTH: 7560
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: p3e1.zhs/opd
US-08-844-274-20

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Query Match 76.7%: Score 13.8; DB 4; Length 7560;
Best Local Similarity 88.2%: Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttct 17
||||| |||||
Db 4357 cgttaatcgcttct 4373

RESULT 12

US-09-251-645-1
; Sequence 1, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9717
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (412)..(1665)
; OTHER INFORMATION: orf1 -46.4 kDa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1686)..(2447)
; OTHER INFORMATION: orf2 -28.1kDa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2758)..(3318)
; OTHER INFORMATION: orf3 -20.7 kDa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3342)..(4118)
; OTHER INFORMATION: orf4 -28.7 kDa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4515)..(9269)
; OTHER INFORMATION: orf5 -176 kDa
US-09-251-645-1

Query Match 76.7%: Score 13.8; DB 4; Length 9717;
Best Local Similarity 88.2%: Pred. No. 93;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttct 17
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Db 546 cgttaatcgcttct 562

RESULT 13

US-07-972-791-1/c
; Sequence 1, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING

;; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PRAVEL, GAMBRELL, HEMITT, & KRISGER
;; STREET: 1177 West Loop South, 10th floor
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA

;; ZIP: 77027
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/972,791
;; FILING DATE: 19921106
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ketelberger, Denise M.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-850-0909
;; TELEFAX: 713-850-0165
;; TELEX: 792026
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3378 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-07-972-791-1

Query Match 75.6%: Score 13.6; DB 1; Length 3378;
Best Local Similarity 92.9%: Pred. No. 11e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
|||||
Db 1519 gtaattcgcttc 1506

RESULT 14
US-09-139-617-10/c
; Sequence 10, Application US/09139617
; Patent No. 6222015
; GENERAL INFORMATION:
; APPLICANT: WILKINSON, HILARY
; TITLE OF INVENTION: ESTROGEN RECEPTOR
; FILE REFERENCE: 20047Y
; CURRENT APPLICATION NUMBER: US/09/139,617
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/058,271
; EARLIER FILING DATE: 1997-09-08
; EARLIER APPLICATION NUMBER: 60/060,520
; EARLIER FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: HUMAN
US-09-139-617-10

Query Match 73.3%: Score 13.2; DB 4; Length 23;
Best Local Similarity 83.3%: Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgttaatcgcttc 18
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Db 19 cgttaatcgcttc 2

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RESULT 15
US-09-181-183-1
; Sequence 1, Application US/09181183
; Patent No. 6146866
; GENERAL INFORMATION:
; APPLICANT: VITANEN, PAUL VEIKKO
; APPLICANT: BACOT, KAREN ONLEY
; APPLICANT: JORDAN, DOUGLAS BRIAN
; TITLE OF INVENTION: LUMAZINE SYNTHASE AND
; TITLE OF INVENTION: RIBOFLAVIN SYNTHASE
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,183
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE//DOCKET NUMBER: CL-1083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: mature spinach LS
; US-09-181-183-1

Query Match 73.3%; Score 13.2; DB 3; Length 471;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||
Db 276 CGTTAATTCTGCTTCTC 293
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Search completed: August 21, 2002, 22:12:32
Job time: 5705 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sv model

Run on: August 21, 2002, 21:32:20 : Search time 5019.06 Seconds

(Without alignments)
48.405 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgccgtctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
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8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	15.4	85.6	277	12	BH452985 B0MGA60TF
C 3	15.4	85.6	493	12	AZ498171 1M0335P13
C 4	15.4	85.6	499	12	BH144783 TDBE091TH
C 5	15.4	85.6	740	12	AG042918 Pan trogl
C 6	15.4	83.3	311	9	AW833312
C 7	15.4	83.3	543	10	BI881942 fms9912.x
C 8	15.4	83.3	636	10	BE557132 fkg9409.Y
C 9	15.4	83.3	728	10	BE557132 fkg9409.Y
C 10	15.4	83.3	1057	12	AC081712 Pan trogl
C 11	14.8	82.2	206	12	AZ891070
C 12	14.8	82.2	206	12	AZ891080 2M0275P03
C 13	14.8	82.2	303	9	AA785231
C 14	14.8	82.2	388	10	BF490378 AT6884.5
C 15	14.8	82.2	398	10	BE95152 UT-M-CG0P
C 16	14.8	82.2	411	9	AI869164 w15b04.x
C 17	14.8	82.2	426	9	AI212546 x8b12a1.f

18	14.8	82.2	430	9	AI946050	AI946050 bs20B03.Y
19	14.8	82.2	448	12	AQ945783	AQ945783 Sheared D
20	14.8	82.2	457	10	BM130898	BM130898 p10h10.Y
21	14.8	82.2	463	10	BM130858	BM130858 p10e01.Y
C 22	14.8	82.2	464	9	AA941852	AA941852 LD27162.5
C 23	14.8	82.2	481	10	BM130610	BM130610 p107a11.Y
C 24	14.8	82.2	484	12	BH378699	BH378699 AG-ND-172
C 25	14.8	82.2	505	10	BM131033	BM131033 p12f08.Y
C 26	14.8	82.2	513	12	AA533012	AA533012 0146b12.s
C 27	14.8	82.2	509	12	CNS07137	AL611857 Anopheles
C 28	14.8	82.2	527	10	BM130436	BM130436 p105a04.Y
C 29	14.8	82.2	574	9	AI488250	AI488250 EST246572
C 30	14.8	82.2	578	10	BF491977	BF491977 AT28836.5
C 31	14.8	82.2	585	10	BI984526	BI984526 fu03g07.Y
C 32	14.8	82.2	594	10	BE978242	BE978242 bs75h01.Y
C 33	14.8	82.2	598	12	AO657044	AO657044 Sheared D
C 34	14.8	82.2	615	12	AO733407	AO733407 HS_5550.B
C 35	14.8	82.2	642	9	AI657509	AI657509 AEMTC24
C 36	14.8	82.2	651	9	AI108056	AI108056 GH06775.5
C 37	14.8	82.2	651	9	AI237983	AI237983 GH13914.5
C 38	14.8	82.2	671	10	BF486076	BF486076 AT20239.5
C 39	14.8	82.2	707	10	BF504348	BF504348 AT05693.5
C 40	14.8	82.2	726	10	BF485588	BF485588 AT19512.5
C 41	14.8	82.2	733	10	BF494223	BF494223 AT02664.5
C 42	14.8	82.2	745	10	BF491456	BF491456 AT28196.5
C 43	14.8	82.2	750	10	BF493859	BF493859 AT02228.5
C 44	14.8	82.2	804	10	BF382280	BF382280 601815190
C 45	14.8	82.2	860	12	CNS04KCL	AL294654 Tetraodon

ALIGNMENTS

RESULT 1
AZ359925 262 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0103B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0103B02 F, DNA sequence.
ACCESSION AZ359925
VERSION AZ359925.1 GI:10473625
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std error: 0.00
Plate: 0103 row: B column: 02
Seq primer: CGTTGTAAACGACGCGCGGT
Class: plasmid ends
High quality sequence stop: 262.
Location/Qualifiers
1..262
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0103B02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

FEATURES
source

/sex="Male"
/lab.host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 97 a 42 c 72 g 51 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 262;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gtaattcgagctctc 18
|||||
Db 214 GTTAATCGCCTCTC 198

RESULT 2
BH452985/c 277 bp DNA linear GSS 12-DEC-2001
LOCUS BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, DNA
DEFINITION
sequence.
ACCESSION BH452985
VERSION BH452985.1 GI:17638696
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 277)
Town, C.D., Van Aken, S., Uterback, T., and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
unpublished (2001)
Other_GSSs: BOHGA60TR
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source Location/Qualifiers
1..277
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHGA60"
/clone_1lb="BOHG"
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 82 a 79 c 66 g 50 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 277;
Best Local Similarity 94.1%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 cgttaattcgagctctc 17
|||||
Db 94 CGTTAATCGCCTTCT 78

RESULT 3
A2498171/c 493 bp DNA linear GSS 05-OCT-2000
LOCUS A2498171/c
DEFINITION
1M0335P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0335P13 F, DNA sequence.
ACCESSION A2498171
VERSION A2498171.1 GI:10675786
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 493)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 385 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0335 row: P column: 13
Seq primer: CGTTCGMAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 493.

FEATURES
source Location/Qualifiers
1..493
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0335P13"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab.host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 141 a 86 c 136 g 130 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 493;
 Best Local Similarity 94.1%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgtctc 18
 ||||||| |||||
 Db 383 GTTAATTCGCTCTC 367

RESULT 4
 BHI44783 499 bp DNA linear GSS 16-AUG-2001
 LOCUS TDE0917H CT0G Lycopersicon esculentum genomic clone CT0G30P13, DNA
 DEFINITION sequence.
 BHI44783
 ACCESSION BHI44783.1 GI:15200046
 VERSION
 KEYWORDS GSS.
 SOURCE Lomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; easterids I; Solanales; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 499)
 van der Hoeven, R., Sun, H., Cho, J., Utterback, T., Romning, C. and
 Tanksley, S.
 Tomato Demethylated Genomic DNA Sequences
 Unpublished (2001)
 CONTACT: CUGI
 CLEMSON UNIVERSITY Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 Lomato demethylated genomic DNA
 Insert Length: 1270 Std Error: 0.00
 Seq primer: M13P-R
 Class: Shotgun.

FEATURES
 source Location/Qualifiers
 1..499
 /organism="Lycopersicon esculentum"
 /cultivar="E6203"
 /db_xref="taxon:4081"
 /clone="CT0G30P13"
 /clone_1lb="CT0G"
 /tissue_type="young leaves"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="E.coli JM109"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; This library was made from short EcoRI digested
 fragments of the genome of Lycopersicon esculentum ligated
 into pBS (SK-). The fragments were cloned into the
 methylation restrictive E.coli strain JM109 with the
 purpose of enriching the library for non-methylated DNA
 fragments. This procedure may enrich the pool of cloned
 fragments in JM109 cells for sequences representing
 expressed genes. Average insert size 1.27 kb."
 BASE COUNT 152 a 108 c 82 g 157 t
 ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 499;
 Best Local Similarity 94.1%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgtctc 18
 ||||||| |||||
 Db 116 GTTAATTCGCTCTC 132

RESULT 5
 AG042918

LOCUS AG042918 740 bp DNA linear GSS 01-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-021B05.R, genomic survey sequence.
 AG042918
 AG042918.1 GI:16571643
 VERSION
 GSS: GSS (genome survey sequence).
 KEYWORDS Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
 SOURCE BAC library clone:PTB-021B05.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 1 (sites)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 740)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpses@sc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13Rev
 LIBRARY
 Vector : PKS145
 R.Site 1 : SacI
 R.Site 2 : SacI
 Location/Qualifiers
 1..740
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-021B05.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_1lb="PTB Chimpanzee Male BAC Library"
 BASE COUNT 242 a 129 c 118 g 236 t 15 others
 ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 740;
 Best Local Similarity 94.1%; Pred. No. 6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgtctc 18
 ||||||| |||||
 Db 614 GTTAATTCGCTCTC 630

RESULT 6
 AM833312 311 bp mRNA linear EST 18-MAY-2000
 LOCUS RC2-TT0007-011199-011-h07 TT0007 Homo sapiens cDNA, mRNA sequence.
 AM833312
 AM833312.1 GI:7927286
 VERSION
 EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 311)
 Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
MEDLINE
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICH Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC2-TT0007-011
199-011-h076t3-1999-11-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 69.
Location/Qualifiers

FEATURES

SOURCE

1. 311
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="TT0007"

/dev_stage="Adult"

/note="Organ: testis; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 83 a 52 c 105 g 71 t
ORIGIN

Query Match 83.3%; Score 15; DB 9; Length 311;
Best Local Similarity 100.0%; Pred. No. 7,9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ttaatcgcttcctc 18
|||||
Db 245 TTAATCGCTTCCTC 231

RESULT 7

LOCUS B1881942 543 bp mRNA linear EST 12-OCT-2001
DEFINITION fmb9912.x1 zebrafish Research Genetics C32 fin Danilo rerio cDNA
clone 4468054 3' similar to TR:Q9Y4U4 Q9Y4U4 HYPOTHETICAL 164.5 KD
PROTEIN: mRNA sequence.

ACCESSION B1881942
VERSION B1881942.1 GI:16089213
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danilo rerio

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 543)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Washu zebrafish EST Project 1998
Unpublished (1998)
Other_ESTS: fmb9912.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

Email: zbrfish@watson.wustl.edu
CDNA Library Preparation: Ning Wu. CDNA Library Arrayed by: Steve
Johnson. DNA Sequencing by: Washington University Genome Sequencing
Center. Cloning distribution: Research Genetics web address:
http://www.researchgenetics.com/
Seq primer: T7 from Gibco
High quality sequence stop: 447.
Location/Qualifiers

1. 543
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_id="4468054"
/clone_lib="zebrafish Research Genetics C32 fin"
/issue_type="Fin"
/lab_host="Genethogs (HS996, a phage-resistant isolate of
DH10B)."

/note="Vector: pT7T3D-Pac with a modified polylinker;
Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared
from zebrafish(C32) fin, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is non-normalized. Library was
constructed by Ning Wu. NOTE: Clones from this library are
only available thru Research Genetics (www.resgen.com)."

BASE COUNT 203 a 88 c 91 g 161 t
ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 543;
Best Local Similarity 100.0%; Pred. No. 9,1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ttaatcgcttcctc 17
|||||
Db 96 TTAATCGCTTCCTC 110

RESULT 8

LOCUS BE557132 636 bp mRNA linear EST 30-AUG-2000
DEFINITION fK94G09.y1 zebrafish Research Genetics C32 fin Danilo rerio cDNA 5'
similar to TR:O75923 O75923 DYSFERLIN.; mRNA sequence.

ACCESSION BE557132
VERSION BE557132.1 GI:9821557
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danilo rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 636)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Washu zebrafish EST Project 1998
Unpublished (1998)
Other_ESTS: fK94G09.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

TITLE
JOURNAL
COMMENT

Email: zbrfish@watson.wustl.edu
CDNA Library Preparation: Ning Wu. CDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University Genome
Sequencing Center. Cloning distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T7 ET from Amersham
High quality sequence stop: 450.

```

FEATURES
source
    Location/Qualifiers
    1..636
    /organism="Danio rerio"
    /db_xref="taxon:7955"
    /clone_lib="Zebrafish Research Genetics C32 fin"
    /tissue_type="Fin"
    /lab_host="GeneHogs (HS996, a phage-resistant isolate of DH10B)"
    /note="Vector: pRTT3D-Pac with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: Clones from this library are only available thru Research Genetics (www.resgen.com)."
```

BASE COUNT 203 a 129 c 114 g 190 t

ORIGIN

```

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 636;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 3 ttaattcgcttcct 17

DB 18 ttaattcgcttcct 32

```

RESULT 9
BG723264 728 bp mRNA linear EST 08-MAY-2001
LOCUS 6026908841 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823109 5',
DEFINITION mRNA sequence.
ACCESSION BG723264
VERSION BG723264.1 GI:14002451
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 728)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palakovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://lmnl0732.row.h column: 22
Plate: LLM10732
High quality sequence stop: 725.
Location/Qualifiers
1..728
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4823109"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: BluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-ttttttttttttttttt-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
```

```

BASE COUNT 126 a 224 c 236 g 142 t
ORIGIN
    Institutes of Health). Note: this is a NIH_MGC Library."
```

Query Match 83.3%; Score 15; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ttaattcgcttcct 18

DB 550 ttaattcgcttcct 536

```

RESULT 10
AG081712
LOCUS AG081712 1057 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-078G04.R, genomic survey sequence.
ACCESSION AG081712
VERSION AG081712.1 GI:16633514
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone: PTB-Chimpanzee Male
BAC Library clone: PTB-078G04.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (sites)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 1057)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..1057
/organism="Pan troglodytes"
/db_xref="taxon:9596"
/clone="PTB-078G04.R"
/sex="male"
/cell_type="Lymphoblast"
/clone_lib="PTB-Chimpanzee Male BAC Library"
BASE COUNT 233 a 232 c 383 g 175 t 34 others
ORIGIN
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Query Match 83.3%; Score 15; DB 12; Length 1057;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttcct 16

DB 890 gtaattcgcttcct 904

```

RESULT 11
A2991070 206 bp DNA linear GSS 27-APR-2001
LOCUS A2991070
```

DEFINITION 2M0275N03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION A2991070
VERSION A2991070
KEYWORDS GI:13862297
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 206)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: N column: 03
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 206.
Location/Qualifiers
1. 206
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275N03"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 47 a 69 c 44 g 46 t
ORIGIN

Query Match 82.2% Score 14.8; DB 12: Length 206;
Best Local Similarity 88.9% Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
||||| ||| |||||
Db 115 CGTTATTCGCGCTTCCTC 132

RESULT 12
A2991080

LOCUS A2991080 206 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0275P03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION A2991080
VERSION A2991080
KEYWORDS GI:13862307
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 206)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: P column: 03
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 206.
Location/Qualifiers
1. 206
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275P03"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 48 a 69 c 44 g 45 t
ORIGIN

Query Match 82.2% Score 14.8; DB 12: Length 206;
Best Local Similarity 88.9% Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
||||| ||| |||||
Db 115 CGTTATTCGCGCTTCCTC 132

RESULT 13

AA785231 303 bp mRNA linear EST 29-JUL-1998
 LOCUS 9508a1.f1 Aspergillus nidulans 24hr asexual developmental and
 DEFINITION vegetative cDNA lambda zap library Emericella nidulans cDNA clone
 9508a1 3', mRNA sequence.
 ACCESSION AA785231 GI:2845399
 VERSION
 SOURCE
 KEYWORDS
 ORGANISM
 EST.
 Emericella nidulans.
 Emericella nidulans
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; Emericella.
 1 (bases 1 to 303)
 Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
 Prade,R. and Roe,B.
 An Aspergillus nidulans EST Database
 Unpublished (1998)
 Other-ESTs: 9508a1.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Partington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 We anticipate the future release of the cDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: M13-20
 High quality sequence stop: 185.
 Location/Qualifiers
 1..303
 /organism="Emericella nidulans"
 /strain="FGSC A26"
 /db_xref="taxon:162425"
 /clone="9508a1"
 /clone_lib="Aspergillus nidulans 24hr asexual
 developmental and vegetative cDNA lambda zap library"
 /tissue_type="vegetative mycelia, asexual structures"
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pluscript
 3' end of cDNA cloned into XhoI site of pBluescript"
 BASE COUNT 85 a 90 c 65 g 63 t
 ORIGIN

Query Match 82.2%; Score 14.8; DB 9; Length 303;
 Best Local Similarity 88.9%; Pred. No. 1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaattcgctctc 18
 1 ||||| ||||| |||||
 Db 87 CTTTAAATCCGCTTCCTC 104

RESULT 14
 BF490378 388 bp mRNA linear EST 23-APR-2001
 LOCUS AT26843.5prtime AT Drosophila melanogaster adult testes potb7
 DEFINITION Drosophila melanogaster cDNA clone AT26843 5 similar to CG7251:
 F8an0007251 located on: 2L 25F1-25F1; 04/09/2001, mRNA sequence.
 ACCESSION BF490378 GI:13756100
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 388)
 Stapleton,M., Brokslein,P., Hong,L., Agbayani,A., Baxter,E., Berman
 ,B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan
 ,D., Friese,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P.,
 Liao,G., Miranda,A., Mista,S., Mungall,C.J., Nunoo,J., Pacleb,J.,

Paragas,V., Park,S., Phouanemavong,S., Wan,K., Yu,C., Lewis,S.E.,
 Celniker,S. and Rubin,G.M.
 BDGP/HMT AT Drosophila EST Project
 Unpublished (2000)
 On Dec 6, 2000 this sequence version replaced g1.11573689.
 COMMENT
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 hit genomic AE003610: arm:2L [5357975,5614606]
 estimated-cyto:25E2-25F4: 04/09/2001
 Plate: AT.268 row: D column: 7
 High quality sequence stop: 334.
 Location/Qualifiers
 1..388
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="AT26843"
 /clone_lib="AT Drosophila melanogaster adult testes potb7"
 /sex="male"
 /dev_stage="0-3 day old Ore-R males"
 /lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
 AT.121-AT.319: DH5-alpha TONA"
 /note="Organ: ADUR testes; Vector: potb7; Site.1: EcoRI;
 Site.2: XhoI; The mRNA for the testis library was made
 from testes and seminal vesicles hand dissected from 0-3
 day old Ore-R males. RNA kindly provided by the lab of
 Margaret Fuller. Sized fractionated cDNAs were directly
 ligated into potb7. Plasmid cDNA library."
 BASE COUNT 103 a 109 c 85 g 91 t
 ORIGIN

Query Match 82.2%; Score 14.8; DB 10; Length 388;
 Best Local Similarity 88.9%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaattcgctctc 18
 1 ||||| ||||| |||||
 Db 82 CTTTAAATCCGCTTCCTC 99

RESULT 15
 BE995152/c 398 bp mRNA linear EST 05-OCT-2000
 LOCUS UI-M-CG0P-b11-g-02-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 DEFINITION UI-M-CG0P-b11-g-02-0-UI 3', mRNA sequence.
 ACCESSION BE995152
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.
 1 (bases 1 to 398)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL 97044477
 MEDLINE
 CONTACT: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the retina tissue cDNA library preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 1-22,
>AT-rich#low_complexity
Seq primer: M13 Forward
POLYA=yes.

FEATURES

Source

Location/Qualifiers
1. .398
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U1-M-CG0P-D11-9-02-0-01"
/clone_lib="NIH BMAP Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIH_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTCAGCGCCGAC"

BASE COUNT 73 a 96 c 137 g 91 t 1 others
ORIGIN

Query Match 82.2%; Score 14.8; DB 10; Length 398;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcgcttcctc 18
||||| ||| |||||
DB 42 CGTTAATCGCGCTTCCTC 25

Search completed: August 21, 2002, 21:32:27
Job time: 12526 sec